

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 3, 2003, 14:09:36 ; Search time 22 Seconds
(without alignments)
1551.260 Million cell updates/sec

Title: US-09-492-028-2

Perfect score: 1828

Sequence: 1 MAGCCCLSAEKEKESQISAE.....VFAAVKDTILQLNREFNLV 355

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1828	100.0	355	2 A41534	GTP-binding protei
2	1780	97.4	355	2 A40891	GTP-binding protei
3	1538	84.1	359	1 RQMSQ	GTP-binding regula
4	1527	83.5	359	2 S30359	GTP-binding regula
5	1519	83.1	359	2 S71963	GTP-binding protei
6	1518	83.0	353	2 B40891	GTP-binding regula
7	1518	83.0	359	1 RGHUCY	GTP-binding regula
8	1517	83.0	359	2 S45700	G-alpha-11 protein
9	1512	82.7	359	1 RQMS11	GTP-binding regula
10	1502	82.2	359	2 S45699	GTP-binding regula
11	1408	77.0	355	2 T15248	hypothetical prote
12	1406	76.9	353	2 S34347	GTP-binding regula
13	1382.5	75.6	354	2 S33309	GTP-binding regula
14	1332.5	72.9	360	2 JN0115	GTP-binding regula
15	1022	55.9	374	2 B41534	GTP-binding protei
16	1013	55.4	374	2 A41096	GTP-binding regula
17	910.5	49.8	354	1 RGHUO2	GTP-binding regula
18	905.5	49.5	354	1 RGHYO2	GTP-binding regula
19	899.5	49.2	354	1 RQMSO2	GTP-binding regula
20	899.5	49.2	354	2 S27014	GTP-binding regula
21	897.5	49.1	354	1 RGF02	GTP-binding regula
22	895	49.0	355	2 I50238	Gi2 protein alpha-
23	894.5	48.9	354	1 RGRTO2	GTP-binding regula
24	894.5	48.9	354	1 RQKLOA	GTP-binding regula
25	894	48.9	355	1 RGTI2	GTP-binding regula
26	893	48.9	355	2 A61031	GTP-binding regula
27	893	48.9	355	2 S28158	GTP-binding regula
28	892.5	48.8	354	1 RGHUI1	GTP-binding regula
29	892.5	48.8	354	1 RGHUI1	GTP-binding regula

ALIGNMENTS

RESULT 1

A41534

GTP-binding protein alpha-14 chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 02-Feb-2001

C:Accession: A41534; E33833

R:Wilkie, T.M.; Scherle, P.A.; Strathmann, M.P.; Slepak, V.Z.; Simon, M.I.

Proc. Natl. Acad. Sci. U.S.A. 88, 10049-10053, 1991

A:Title: Characterization of G-protein alpha subunits in the G-q class: expression in

A:Reference number: A41534; MUID:92052208; PMID:1946421

A:Accession: A41534

A:Molecule type: mRNA

A:Residues: 1-355 <WIL>

A:Cross-references: GB:M80631; NID:g193568; PIDN:AAA83222.1; PID:g193569

R:Strathmann, M.; Wilkie, T.M.; Simon, M.I.

Proc. Natl. Acad. Sci. U.S.A. 86, 7407-7409, 1989

A:Title: Diversity of the G-protein family: sequences from five additional alpha-subu

A:Reference number: A33833; MUID:90017488; PMID:2508088

A:Accession: E33833

A:Molecule type: mRNA

A:Residues: 217-267 <STR>

A:Cross-references: GB:M57616; NID:g193380; PIDN:AAA63304.1; PID:g193381; GB:M26739

C:Superfamily: GTP-binding regulatory protein Gs alpha chain

C:Keywords: GTP binding; nucleotide binding; p-loop

F:42-49/Region: nucleotide-binding motif A (p-loop)

F:152-154/Region: GTP-binding SAK/L motif

F:270-273/Region: GTP-binding NKXD motif

Query Match 100.0% Score 1828; DB 2: Length 355;
Best Local Similarity 100.0%; Pred. No. 1.7e-132;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCCLSAEKEKESQISAEIERHVRDKDARRELKLLLTGTGSGKSTFKQMRIHG 60

|||||

Db 1 MAGCCCLSAEKEKESQISAEIERHVRDKDARRELKLLLTGTGSGKSTFKQMRIHG 60

|||||

QY 61 SGYSDEDRKGFYKLVYQNIFTAQAMIRAMDTLRTQYMCQENKNAQITREVEVDKVTAL 120

|||||

Db 61 SGYSDEDRKGFYKLVYQNIFTAQAMIRAMDTLRTQYMCQENKNAQITREVEVDKVTAL 120

|||||

QY 121 SRDQVAAIKQLWLDPGIQCYDRRREYQLSDSAKYLTDIRIAMPSPFVPTQDVLVRV 180

|||||

Db 121 SRDQVAAIKQLWLDPGIQCYDRRREYQLSDSAKYLTDIRIAMPSPFVPTQDVLVRV 180

|||||

QY 181 PTTGTIIEYFPDLENIIFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECN 240

|||||

Db 181 PTTGTIIEYFPDLENIIFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECN 240

|||||

QY 241 ENRMEEKALFRTIITYPFWLNSSVILFNKKDLLEEKIMYSHLISYFPEYTCPKQDVKA 300

|||||

Db 241 ENRMEEKALFRTIITYPFWLNSSVILFNKKDLLEEKIMYSHLISYFPEYTCPKQDVKA 300

|||||

QY 301 ARDFILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
|||||
Db 301 ARDFILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355

RESULT 2
A40891
GTP-binding protein G11 alpha chain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 02-Feb-2001
C:Accession: A40891
R:Nakamura, F.; Ogata, K.; Shiozaki, K.; Kameyama, K.; Ohara, K.; Haga, T.; Nukada, T.
J. Biol. Chem. 266, 12676-12681, 1991
A:Title: Identification of two novel GTP-binding protein alpha-subunits that lack apparent
A:Reference number: A40891; MUID:91286303; PMID:1905731
A:Accession: A40891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <NAK>
A:CROSS-references: GB:D90335; NID:g217565; PID:BA414349.1; PID:g217566
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop
F:42-49/Region: nucleotide-binding motif A (P-loop)
F:152-154/Region: GTP-binding SAK/L motif
F:270-273/Region: GTP-binding NKXD motif

Query Match 97.4%; Score 1780; DB 2; Length 355;
Best Local Similarity 96.6%; Pred. No. 8e-129;
Matches 343; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAGCCLSAEKESQRTSAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHG 60
|||||
Db 1 MAGCCLSAEKESQRTSAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHG 60

QY 61 SGYSDEDRKGTFLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTAL 120
|||||
Db 61 SGYSDEDRKGTFLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTAL 120

QY 121 SRQOVAIKQLWDPGQIECYDRRREYQVLSAKYLTDIRIAMPSPVPTQDDVLRVRV 180
|||||
Db 121 SRQOVAIKQLWDPGQIECYDRRREYQVLSAKYLTDIRIAMPSPVPTQDDVLRVRV 180

QY 181 PTTGITEYFDLENIFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECND 240
|||||
Db 181 PTTGITEYFDLENIFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECND 240

QY 241 ENRMESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYFPYTGPKQDVKA 300
|||||
Db 241 ENRMESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYFPYTGPKQDVKA 300

QY 301 ARDFILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
|||||
Db 301 ARDFILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355

RESULT 3
RGM5Q
GTP-binding regulatory protein Gq alpha chain - mouse
N:Alternate names: guanine nucleotide binding protein Gq alpha chain; heterotrimeric G-protein
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001
C:Accession: A38414
R:Strathmann, M.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 87, 9113-9117, 1990
A:Title: G protein diversity: a distinct class of alpha subunits is present in vertebrates
A:Reference number: A38414; MUID:91067657; PMID:2123549
A:Accession: A38414
A:Molecule type: mRNA
A:Residues: 1-359 <STR>
A:CROSS-references: GB:M55412; NID:g193501; PID:AA63306.1; PID:g193502
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
signals. The beta and gamma chains, required for GTPase activity, appear to be common to all
types; it is specific for each type of G protein.

C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction
F:46-53/Region: nucleotide-binding motif A (P-loop)
F:274-277/Region: GTP-binding NKXD motif
F:52/Binding site: GTP (lys) #status predicted
F:183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 84.1%; Score 1538; DB 1; Length 359;
Best Local Similarity 82.3%; Pred. No. 2.8e-110;
Matches 289; Conservative 34; Mismatches 28; Indels 0; Gaps 0;

QY 5 CCLSAEKEESQRTSAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHGSGYS 64
|||||
Db 9 CCLSEAEKARRINDETERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHGSGYS 68

QY 65 DEDRKGTFLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTALSRDQ 124
|||||
Db 69 DEDRKGTFLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTALSRDQ 128

QY 125 VAATKQLWDPGQIECYDRRREYQVLSAKYLTDIRIAMPSPVPTQDDVLRVRVPTTG 184
|||||
Db 129 VDAIKSLWDPGQIECYDRRREYQVLSAKYLTDIRIAMPSPVPTQDDVLRVRVPTTG 188

QY 185 IIEYFPDLENIFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECNDENRM 244
|||||
Db 189 IIEYFPDQSVIFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECNDENRM 248

QY 245 EESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYFPYTGPKQDVKAARD 304
|||||
Db 249 EESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYFPYTGPKQDVKAARD 308

QY 305 ILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
|||||
Db 309 ILKMEVDLNPDSKLIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 359

RESULT 4
S30359
GTP-binding regulatory protein G alpha chain, phospholipase C-activating - turkey
N:Alternate names: phospholipase C-activating G protein
C:Species: Meleagris gallopavo (common turkey)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Feb-2001
C:Accession: S30359; S30360
R:Maurice, D.H.; Waldo, G.L.; Morris, A.J.; Nicholas, R.A.; Harden, T.K.
Biochem. J. 290, 765-770, 1993
A:Title: Identification of Galpha(11) as the phospholipase C-activating G-protein of
Biochem. J. 290, 765-770, 1993
A:Reference number: S30359; MUID:93207527; PMID:8457205
A:Accession: S30359
A:Molecule type: mRNA
A:Residues: 1-359 <MAU>
A:CROSS-references: GB:X73072; NID:g312254; PID:CAA51530.1; PID:g312255
A:Experimental source: blood
A:Accession: S30360
A:Molecule type: protein
A:Residues: 78-92;121-132;158-180;253-256;307-312;339-345;355-359 <MAU>
A:Experimental source: erythrocytes
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop
F:46-53/Region: nucleotide-binding motif A (P-loop)
F:156-158/Region: GTP-binding SAK/L motif
F:274-277/Region: GTP-binding NKXD motif
F:52/Binding site: GTP (lys) #status predicted
F:183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 83.5%; Score 1527; DB 2; Length 359;
Best Local Similarity 82.1%; Pred. No. 1.9e-109;
Matches 288; Conservative 36; Mismatches 27; Indels 0; Gaps 0;

QY 5 CCLSAEKEESQRTSAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHGSGYS 64
|||||
Db 9 CCLSDVKEKSRINAEIQRLRRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHGSGYS 68

QY 65 DEDRKGTFLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTALSRDQ 124

Db 69 EEDKRGFTKLIVYQNIPTAMQSMIRAMETLKIILYKEONKANAVLIREVDVEKVMTFEQPY 128
QY 125 VAAIKOLWLDPGIQECYDRRREVQLSDSAKYLYLTDTIERIAMPSEFVPTQODVLRVVRPTTG 184
Db 129 VSAIKTLWMDPGIQECYDRRREVQLSDSAKYLYLSDVRIATFGYLTQODVLRVVRPTTG 188
QY 185 IIEYPPDLENIIFRMVMDVGGQSRERKWIHCFESVTSIIFLVLSYDQVLAECQENRM 244
Db 189 IIEYPPDLENIIFRMVMDVGGQSRERKWIHCFENVTSMFLVLSYDQVLAECQENRM 248
QY 245 EESKALFRITIIYPWFLNSVILFNKKDLLEEKIMYSHLISYFPYTPGPKQDVKAARDP 304
Db 249 EESKALFRITIIYPWFLNSVILFNKKDLLEEKIMYSHLISYFPYTPGPKQDVKAARDP 308
QY 305 ILKLYDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 309 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 359

RESULT 5
S71963
GTP-binding protein alpha-q - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C:Accession: S71963
R:Johnson, G.J.; Leis, L.A.; Dunlop, P.C.
Biochem. J. 318, 1023-1031, 1996
A:Title: Specificity of G-alpha(q) and G-alpha(11) gene expression in platelets and erythrocytes
A:Reference number: S71963; MUID:96433124; PMID:8836152
A:Accession: S71963
A:Molecule type: mRNA
A:Residues: 1-359 <OH>
A:Cross-references: EMBL:L76256; NID:g1478071; PIDN:AAB39498.1; PID:g1478072
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F:46-53/Region: nucleotide-binding motif A (P-loop)
F:274-277/Region: GTP-binding NKXD motif

Query Match 83.1%; Score 1519; DB 2; Length 359;
Best Local Similarity 81.2%; Pred. No. 7.9e-109;
Matches 285; Conservative 36; Mismatches 30; Indels 0; Gaps 0;

QY 5 CCLSAEKEQSQRISAEIERHVRDKKARRELKLLLLGTGSGKSTFIKQMRIIHGSGYS 64
Db 9 CCLSEAEKARRINDEIERQLRRDKRDRRELKLLLLGTGSGKSTFIKQMRIIHGSGYS 68
QY 65 DEDKRGFTKLIVYQNIPTAMQSMIRAMDTLRIQIMCEQNKENAIQIREVEVDKVTALSRDQ 124
Db 69 DEDKRGFTKLIVYQNIPTAMQSMIRAMDTLKIPIKYEHKHAQLVREVDEKVSAPENPY 128
QY 125 VAAIKOLWLDPGIQECYDRRREVQLSDSAKYLYLTDTIERIAMPSEFVPTQODVLRVVRPTTG 184
Db 129 VDAIKSLWMDPGIQECYDRRREVQLSDSTKYLYLNDLRVADPAYLTQODVLRVVRPTTG 188
QY 185 IIEYPPDLENIIFRMVMDVGGQSRERKWIHCFESVTSIIFLVLSYDQVLAECQENRM 244
Db 189 IIEYPPDLSQVIFRMVMDVGGQSRERKWIHCFENVTSMFLVLSYDQVLAECQENRM 248
QY 245 EESKALFRITIIYPWFLNSVILFNKKDLLEEKIMYSHLISYFPYTPGPKQDVKAARDP 304
Db 249 EESKALFRITIIYPWFLNSVILFNKKDLLEEKIMYSHLISYFPYTPGPKQDVKAARDP 308
QY 305 ILKLYDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 309 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 359

RESULT 6
B40891
GTP-binding protein G12 alpha chain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 02-Feb-2001

C:Accession: B40891
R:Nakamura, F.; Ogata, K.; Shiozaki, K.; Kameyama, K.; Ohara, T.; Nukada, T.
J. Biol. Chem. 266, 12676-12681, 1991
A:Title: Identification of two novel GTP-binding protein alpha-subunits that lack app
A:Reference number: A40891; MUID:91286303; PMID:1903731
A:Accession: B40891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-353 <NA>
A:Cross-references: GR:D90336; NID:g217567; PIDN:BAAL4350.1; PID:g217568
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop
F:40-47/Region: nucleotide-binding motif A (P-loop)
F:150-152/Region: GTP-binding SAK/L motif
F:268-271/Region: GTP-binding NKXD motif

Query Match 83.0%; Score 1518; DB 2; Length 353;
Best Local Similarity 81.5%; Pred. No. 9.2e-109;
Matches 286; Conservative 37; Mismatches 28; Indels 0; Gaps 0;

QY 5 CCLSAEKEQSQRISAEIERHVRDKKARRELKLLLLGTGSGKSTFIKQMRIIHGSGYS 64
Db 3 CCLSDVEKSKKINAEIEKQLRRDKRDRRELKLLLLGTGSGKSTFIKQMRIIHGAGYS 62
QY 65 DEDKRGFTKLIVYQNIPTAMQSMIRAMDTLRIQIMCEQNKENAIQIREVEVDKVTALSRDQ 124
Db 63 DEDKRGFTKLIVYQNIPTAMQSMIRAMETLKIILYKEONKANALLIREVDVEKVTFEHRY 122
QY 125 VAAIKOLWLDPGIQECYDRRREVQLSDSAKYLYLTDTIERIAMPSEFVPTQODVLRVVRPTTG 184
Db 123 VSAIKTLWMDPGIQECYDRRREVQLSDSAKYLYLTVDRIATSGYLTQODVLRVVRPTTG 182
QY 185 IIEYPPDLENIIFRMVMDVGGQSRERKWIHCFESVTSIIFLVLSYDQVLAECQENRM 244
Db 183 IIEYPPDLENIIFRMVMDVGGQSRERKWIHCFENVTSMFLVLSYDQVLAECQENRM 242
QY 245 EESKALFRITIIYPWFLNSVILFNKKDLLEEKIMYSHLISYFPYTPGPKQDVKAARDP 304
Db 243 EESKALFRITIVYIPWFLNSVILFNKKDLLEKILHSHLVDFPEFDGPQDAQAAREF 302
QY 305 ILKLYDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 303 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 353

RESULT 7
RGHUGY
GTP-binding regulatory protein Gy alpha chain - human
N:Alternate names: guanine nucleotide binding protein Gy alpha chain; heterotrimeric
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001
C:Accession: A39394
R:Jiang, M.; Pandey, S.; Tran, V.T.; Fong, H.K.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 3907-3911, 1991
A:Title: Guanine nucleotide-binding regulatory proteins in retinal pigment epithelial
A:Reference number: A39394; MUID:91219481; PMID:1902575
A:Accession: A39394
A:Molecule type: mRNA
A:Residues: 1-359 <JA>
A:Cross-references: GB:M69013; NID:gl83690; PIDN:AAA58624.1; PID:gl83691
C:Comment: The G proteins are a family of guanine nucleotide-binding proteins that re
ains. The beta and gamma chains, required for GTPase activity, appear to be common to
rase. It is specific for each type of G protein.

C:Genetics: GDB:GNALL
A:Gene: GDB:GNALL
A:Cross-references: GDB:I32587; OMIM:139313
A:Map position: 19p13.3-19p13.3
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transductio
F:46-53/Region: nucleotide-binding motif A (P-loop)
F:274-277/Region: GTP-binding NKXD motif
F:52/Binding site: GTP (Lys) #status predicted
F:183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

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NIKJODA, N.J.F.; FINDLAY, J.B.C.; REID, J.D.

[illegible]

Biochem. J. 292, 333-341, 1993
A:Title: The molecular cloning of the squid (Loligo forbesi) visual Gq-alpha subunit and A:Reference number: S33309; MUID:93277493; PMID:8503868
A:Accession: S33309
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-354 <RVB>
A:Cross-references: EMBL:L10289
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop
F:40-47/Region: nucleotide-binding motif A (P-loop)
F:150-152/Region: GTP-binding SAK/L motif
F:269-272/Region: GTP-binding NKXD motif

Query Match 75.6%; Score 1382.5; DB 2; Length 354;
Best Local Similarity 74.4%; Pred. No. 2.2e-98;
Matches 262; Conservative 37; Mismatches 52; Indels 1; Gaps 1;

QY 5 CCLSAEKEKSORISAEIERHVRDQKDDARRELKLLLLGTGSGKSTFIKOMRIHSGYS 64
Db 3 CCLSEAEKQKRIQETEKQLRRDKDARRELKLLLLGTGSGKSTFIKOMRIHSGYS 62
QY 65 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIREVEVDKVTALSRQ 124
Db 63 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIREVEVDKVTALSRQ 122
QY 125 VAAIKQLWLDPGIQECYDRRREYQLSDSAKYILTDIERIAMPFSVPTQDVLVRVPTTG 184
Db 123 VTAIKGCTWDPGMOECYDRRREYQLTDSAKYILDDVERIHEPGYIPTQLDILVRVPTTG 182
QY 185 IIEYPPDLENIIRPMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECND-ENR 243
Db 183 IIEYPPDLYSIIRPMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLFESDNEENR 242
QY 244 MEESKALFRITIIYPWFQNSVILFLNKKDLEEKIMYSHLISYFPEYTPGKQDVAARD 303
Db 243 MEESKALFRITIIYPWFQNSVILFLNKKDLEEKIMYSHLADYFPDYGPKDYEARE 302
QY 304 FILKLYQDQNPDEKVIYSHFTCATDPTENIRFVFAAVKDTILQNLREFNLV 355
Db 303 FMDSYMDLNEDKEMLYHYTCATDPTENIRFVFAAVKDTILQNLKEYNLV 354

RESULT 14
JN0115
GTP-binding regulatory protein dqg alpha chain - fruit fly (Drosophila melanogaster)
N:Alternate names: dqg protein
C:Species: Drosophila melanogaster
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Feb-2001
C:Accession: JN0115
R:Lee, Y.J.; Dobbs, M.B.; Verardi, M.L.; Hyde, D.R.
Neuron 5, 889-898, 1990
A:Title: dqg: a drosophila gene encoding a visual system-specific G alpha molecule.
A:Reference number: JN0115; MUID:91097801; PMID:2125225
A:Accession: JN0115
A:Molecule type: DNA
A:Residues: 1-360 <LEE>
C:Genetics:
A:Gene: dqg
A:Cross-references: FlyBase:FBgn0004435
A:Introns: 40/1; 101/3; 153/2; 196/2; 239/3; 298/1; 334/1
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: alternative splicing; GTP binding; nucleotide binding; P-loop
F:1-360/Product: GTP-binding regulatory protein dqg alpha chain I #status predicted <MAT>
F:1-297,333-360/Product: GTP-binding regulatory protein dqg alpha chain II #status predicted
F:40-47/Region: nucleotide-binding motif A (P-loop)
F:150-152/Region: GTP-binding SAK/L motif
F:268-271/Region: GTP-binding NKXD motif

Query Match 72.9%; Score 1332.5; DB 2; Length 360;
Best Local Similarity 71.4%; Pred. No. 1.5e-94;
Matches 255; Conservative 39; Mismatches 56; Indels 7; Gaps 1;

QY 5 CCLSAEKEKSORISAEIERHVRDQKDDARRELKLLLLGTGSGKSTFIKOMRIHSGYS 64
Db 3 CCLSEAEKQKRIQETEKQLRRDKDARRELKLLLLGTGSGKSTFIKOMRIHSGYS 62
QY 65 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIREVEVDKVTALSRQ 124
Db 63 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIREVEVDKVTALSRQ 122
QY 125 VAAIKQLWLDPGIQECYDRRREYQLSDSAKYILTDIERIAMPFSVPTQDVLVRVPTTG 184
Db 123 LNAIKTLWDAGIQECYDRRREYQLTDSAKYILDLARIEADYLPTEQDILRARVPTTG 182
QY 185 IIEYPPDLENIIRPMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECNDENRM 244
Db 183 ILSEYPPDLGIVFRMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLFESDNEENRM 242
QY 245 EESKALFRITIIYPWFQNSVILFLNKK-----DLLEKIMYSHLISYFPEYTPGKQD 297
Db 243 EESKALFRITIIYPWFQNSVILFLNKKDLEEKIMYSHLVDYFPDYGPKQD 302
QY 298 VKAARDFILKLYQDQNPDEKVIYSHFTCATDPTENIRFVFAAVKDTILQNLREFNL 354
Db 303 HAAAKQFVLKYLACNPDPERQCYSHFTTATDPTENIKLYCAVKDTIMONALKEFNL 359

RESULT 15
B41534
GTP-binding protein alpha-15 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 02-Feb-2001
C:Accession: B41534
R:Wilkie, T.M.; Scherle, P.A.; Strathmann, M.P.; Slepak, V.2.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 88, 10049-10053, 1991
A:Title: Characterization of G-protein alpha subunits in the G-q class: expression in A:Reference number: A41534; MUID:92052208; PMID:1946421
A:Accession: B41534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <WIL>
A:Cross-references: GB:M80632; NID:g193570; PIDN:AAA37713.1; PID:g193571
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop
F:49-56/Region: nucleotide-binding motif A (P-loop)
F:277-280/Region: GTP-binding NKXD motif

Query Match 55.9%; Score 1022; DB 2; Length 374;
Best Local Similarity 54.8%; Pred. No. 9.6e-71;
Matches 201; Conservative 60; Mismatches 92; Indels 14; Gaps 3;

QY 3 GCC--CLSAEKEKSORISAEIERHVRDQKDDARRELKLLLLGTGSGKSTFIKOMRIHSG 60
Db 8 GCCPWCUTEERKTAARIDQENILLEQKKQEREELKLLLPFGESGKSTFIKOMRIHSG 67
QY 61 SGYSDEDRKGTFLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIREVEVDKVTAL 120
Db 68 VGISEEDRRAFRLIIYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIREVEVDKVTAL 127
QY 121 SRDQVAAIKQLWLDPGIQECYDRRREYQLSDSAKYILTDIERIAMPFSVPTQDVLVRV 180
Db 128 EKPYAVAMQYLRWDAGIRACRYERRERFHLDSAVYVLSHLERISEDSYIPTAQDVLRSR 187
QY 181 PTTGIIETPPDLENIIRPMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECND 240
Db 188 PTTGIIETPPDLENIIRPMVDVGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECND 247
QY 241 ENRMESKALFRITIIYPWFQNSVILFLNKKDLEEKIMYSHLISYFPEYTPGKQDVKA 300
Db 248 ENRMESKALFRITIIYPWFQNSVILFLNKKDLEEKIMYSHLISYFPEYTPGKQDVKA 307
QY 301 ARDFILKLY-----QD--QNPDKEVIYSHFTCATDPTENIRFVFAAVKDTILQNL 348
Db 308 AKSFILDMYRVAVCAEPDQGGKGRARRRFAHFTCATDQSVRSVFKDVRDVSILARY 367

Qy 349 LREFNLY 355
| | | |
Db 368 LDEINLL 374

Search completed: February 3, 2003, 14:12:10
Job time : 23 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 3, 2003, 14:03:46 ; Search time 38 Seconds
(without alignments)
1244.841 Million cell updates/sec

Title: US-09-492-028-2
Perfect score: 1828
Sequence: 1 MAGCCCLSAEKSQRISAE.....VFAAVKDTIQLNLRFNLY 355

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1828	100.0	355	21 AAB15026	Mouse TC-Galphal4
2	1771	96.9	355	22 AAB99076	Human G-protein al
3	1771	96.9	355	23 AAB09285	G protein-coupled
4	1537	84.1	353	23 ABG68591	Mouse G protein al
5	1537	84.1	359	23 ABG68592	Mouse G protein al
6	1335	84.0	359	23 AAM48816	Murine G-protein 6
7	1530	83.7	353	23 ABG68588	Mouse G protein al
8	1530	83.7	359	23 ABG68594	Mouse G protein al
9	1527	83.5	353	23 ABG68585	Mouse G protein al
10	1527	83.5	353	23 ABG68600	Human G protein al

11	1527	83.5	359	23	ABG68584	Mouse G protein al
12	1527	83.5	359	23	ABG68604	Human G protein al
13	1526	83.5	353	23	ABG68587	Human G protein al
14	1526	83.5	359	23	ABG68586	Mouse G protein al
15	1524	83.4	359	23	ABG68610	Human G protein al
16	1524	83.4	359	23	ABB09282	G protein-coupled
17	1522	83.3	359	23	ABG68608	Human G protein al
18	1520	83.2	353	23	AAM48817	Murine G-protein 6
19	1520	83.2	353	23	AAM48818	Murine G-protein 6
20	1520	83.2	353	23	AAM48819	Human G-protein al
21	1519	83.1	353	22	AAB99072	Human G-protein al
22	1519	83.1	353	23	ABG68599	G protein-coupled
23	1519	83.1	353	23	ABB09281	Mouse G protein al
24	1519	83.1	359	23	ABG68593	Mouse G protein al
25	1519	83.1	359	23	ABG68595	Human G protein al
26	1519	83.1	359	23	ABG68598	Human G protein al
27	1518	83.0	353	23	ABG68597	Mouse G protein al
28	1518	83.0	359	22	AAB99071	Human G-protein al
29	1518	83.0	359	22	AAB99073	Human G-protein al
30	1517	83.0	359	20	RAY52705	Human G-alpha-11 p
31	1517	83.0	359	20	AAV29789	Human G-alpha-11 p
32	1516	82.9	359	23	ABG68603	Human G protein al
33	1516	82.9	359	23	ABG68605	Human G protein al
34	1515	82.9	353	23	ABG68607	Human G protein al
35	1515	82.9	359	23	ABG68609	Human G protein al
36	1512	82.7	353	23	ABG68589	Mouse G protein al
37	1512	82.7	359	23	ABG68596	Mouse G protein al
38	1509	82.5	353	23	ABG68601	Human G protein al
39	1509	82.5	359	23	ABG68606	Human G protein al
40	1506	82.4	1276	20	AAV49127	phCar/hmGluR2*Gq15
41	1506	82.4	1276	23	AAO15093	Human phCar/hmGluR
42	1506	82.4	1394	20	AAV49129	pmGluR2/Car*Galpha
43	1506	82.4	1394	23	AAO15095	Human pmGluR2-Car*
44	1506	82.4	1397	20	AAV49134	pmGluR2/Car*Galpha
45	1506	82.4	1397	23	AAO15100	Human pmGluR2-Car*

ALIGNMENTS

RESULT 1	
AAB15026	
ID AAB15026 standard; Protein; 355 AA.	
XX	
AC AAB15026;	
XX	
DT 18-DEC-2000 (first entry)	
XX	
DE Mouse TC-Galphal4 protein.	
XX	
KW Mouse; TC-Galphal4; sensory signal; taste.	
XX	
OS Mus sp.	
XX	
PN WO200044929-A2.	
XX	
PD 03-AUG-2000.	
XX	
PF 26-JAN-2000; 2000WO-US02217.	
XX	
PR 27-JAN-1999; 99US-0117367.	
XX	
PA (RECC) UNIV CALIFORNIA.	
XX	
PI Zuker CS;	
XX	
DR WPI; 2000-499336/44.	
XX	
DR N-PSDB; AAA73739.	
XX	
PT Assaying for compounds that modulate sensory signalling in taste cells,	
PT by determining interactions between the compounds and a sensory cell	
PT specific G-protein alpha subunit polypeptide -	
XX	

PS Claim 1; Page 61-62; 67pp; English.

XX The present invention relates to a method for identifying a compound

CC that modulates sensory signalling in taste cells, comprising contacting

CC the compound with a sensory cell specific G-protein alpha subunit

CC polypeptide. Such a polypeptide is the present sequence, mouse

CC 1c-Galpal4 protein. The compounds identified by the present method

CC may be used by the food and pharmaceutical industries to customize

CC taste as additives for food or medicines so that they taste different

CC when eaten.

XX Sequence 355 AA;

SQ Query Match 100.0%; Score 1828; DB 21; Length 355;

Best Local Similarity 100.0%; Pred. No. 6.9e-173;

Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCCLSAEKEQSRIASAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHG 60

DB 1 MAGCCCLSAEKEQSRIASAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHG 60

QY 61 SGYSDEDRKGFTKLIVYONIFTAQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTAL 120

DB 61 SGYSDEDRKGFTKLIVYONIFTAQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTAL 120

QY 121 SRDQVAAIKQLWLDPGTQECYDRRREYQLSDSAKYIYLTDIRIAMPFSVPTQDVLVRV 180

DB 121 SRDQVAAIKQLWLDPGTQECYDRRREYQLSDSAKYIYLTDIRIAMPFSVPTQDVLVRV 180

QY 181 PTGTIIEYPPDLENIIFRMVVDVGQSRERKWIHCFSVTSIIFLVALSEYDQVLAECDN 240

DB 181 PTGTIIEYPPDLENIIFRMVVDVGQSRERKWIHCFSVTSIIFLVALSEYDQVLAECDN 240

QY 241 ENRMESKALFRTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISVFPEYTGPKODVKA 300

DB 241 ENRMESKALFRTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISVFPEYTGPKODVKA 300

QY 301 ARDFILKLYDQNDPKKEKVIYSHFTCATDPTENIRFVFAAVKDTILQNLNREFNLV 355

DB 301 ARDFILKLYDQNDPKKEKVIYSHFTCATDPTENIRFVFAAVKDTILQNLNREFNLV 355

RESULT 2

AAB99076

ID AAB99076 standard; Protein; 355 AA.

XX AAB99076;

XX 23-AUG-2001 (first entry)

XX Human G-protein alpha subunit 14.

XX G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;

KW gonadotrophin releasing; hormone receptor; hormone dependent cancer;

KW human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; rat; mouse;

KW gene therapy.

XX Homo sapiens.

OS WO200136446-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-GB04385.

XX 17-NOV-1999; 99GB-0027215.

XX (UYBR-) UNIV BRISTOL.

PA McArdle CA;

XX PI WPI; 2001-355607/37.

XX WPI; 2001-355607/37.

PT Use of a vector encoding G-protein coupled receptors for manufacturing

PT medicaments for treating cancer, diseases of cardiovascular system, -

XX nervous system, digestive system, immune system, or muscle diseases

XX Disclosure; Fig 19; 78pp; English.

XX The present invention describes a prodrug comprising a vector encoding a

CC G-protein coupled receptor (GPCR). This can be used in the treatment of

CC diseases, including hormone-dependent cancers, cardiovascular, nervous

CC system, digestive system, immune system, respiratory, skeletal,

CC endocrine, sensory and muscle diseases and disorders. The present

CC sequence is a protein described in the exemplification of the invention.

XX Sequence 355 AA;

SQ Query Match 96.9%; Score 1771; DB 22; Length 355;

Best Local Similarity 96.3%; Pred. No. 3.2e-167;

Matches 342; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAGCCCLSAEKEQSRIASAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHG 60

DB 1 MAGCCCLSAEKEQSRIASAEIERHVRDKKDDARRELKLLLLGTGSGKSTFIKQMRIHG 60

QY 61 SGYSDEDRKGFTKLIVYONIFTAQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTAL 120

DB 61 SGYSDEDRKGFTKLIVYONIFTAQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTAL 120

QY 121 SRDQVAAIKQLWLDPGTQECYDRRREYQLSDSAKYIYLTDIRIAMPFSVPTQDVLVRV 180

DB 121 SRDQVAAIKQLWLDPGTQECYDRRREYQLSDSAKYIYLTDIRIAMPFSVPTQDVLVRV 180

QY 181 PTGTIIEYPPDLENIIFRMVVDVGQSRERKWIHCFSVTSIIFLVALSEYDQVLAECDN 240

DB 181 PTGTIIEYPPDLENIIFRMVVDVGQSRERKWIHCFSVTSIIFLVALSEYDQVLAECDN 240

QY 241 ENRMESKALFRTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISVFPEYTGPKODVKA 300

DB 241 ENRMESKALFRTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISVFPEYTGPKODVKA 300

QY 301 ARDFILKLYDQNDPKKEKVIYSHFTCATDPTENIRFVFAAVKDTILQNLNREFNLV 355

DB 301 ARDFILKLYDQNDPKKEKVIYSHFTCATDPTENIRFVFAAVKDTILQNLNREFNLV 355

RESULT 3

ABB09285

ID ABB09285 standard; Protein; 355 AA.

XX ABB09285;

XX 10-JUL-2002 (first entry)

XX G protein-coupled receptor (GPCR) >G(Y-14) SEQ ID NO:31.

XX Target activated nucleic acid biosensor; signalling moiety; GPCR;

KW nucleic acid sensor; detection; engineering; drug optimisation;

KW G protein-coupled receptor.

XX Homo sapiens.

OS WO200222882-A2.

XX 21-MAR-2002.

XX 13-SEP-2001; 2001WO-US28835.

XX 13-SEP-2000; 2000US-232454P.

XX (ARCH-) ARCHEMIX CORP.

XX Stanton M, Epstein D, Hamaguchi N;

XX WPI; 2002-393977/42.

XX Nucleic acid sensor for detecting target molecule, comprises target
PT molecule activation site and optical signalling unit that changes its
PT optical properties upon allosteric modulation sensor after recognition
PT of target -
XX
PS Example 12; Page 90; 144pp; English.
XX
CC The present invention describes a nucleic acid sensor molecule (I)
CC comprising a target molecule activation site comprising a structure that
CC recognises a target molecule and an optical signalling unit including at
CC least one nucleotide coupled to a signalling moiety that changes its
CC optical properties upon allosteric modulation of (I) following
CC recognition of the target molecule. (I) is useful for detecting a target
CC molecule associated with a pathological condition or genetic alteration.
CC (I) is useful for identifying a drug compound, by identifying a nucleic
CC acid biosensor-based molecule profile of target molecules associated with
CC a disease trait in a patient, administering a candidate compound to the
CC patient, and monitoring changes in the profile. Alternately, the method
CC involves identifying a number of pathway target molecules, administering
CC a candidate compound to a patient having a disease trait, and monitoring
CC changes in the structure, level or activity of two or more of the pathway
CC target molecules using (I). The profile of target molecules or the
CC changes in the structure is compared to the profile of a reference
CC healthy or diseased population. (I) is useful in multiple assays, for the
CC detection of target molecule. (I) is also useful in diagnostic
CC applications and drug optimisation. The present sequence represents a
CC G protein-coupled receptor, which is used in an example from the present
CC invention.
XX
SQ Sequence 355 AA;
Query Match 96.9%; Score 1771; DB 23; Length 355;
Best Local Similarity 96.3%; Pred. No. 3.2e-167;
Matches 342; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 MAGCCCLSAEKEQSRIAEIERHVRDKKARRELKLLLLGTGSGKSTFIKQMRIHG 60
Db 1 MAGCCCLSAEKEQSRIAEIERHVRDKKARRELKLLLLGTGSGKSTFIKQMRIHG 60
QY 61 SGYSDEDRGFTKLVYQNIIFTAQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTAL 120
Db 61 SGYSDEDRGFTKLVYQNIIFTAQAMIRAMDTLRIQYVCEQNKNAQIIREVEVDKVTAL 120
QY 121 SRDQVAIAIKQLWDPGIGQECYDRRREYQLSDSAKYIYLTDIRTAMPSFVPTQDDVLRVRV 180
Db 121 SRQVFAIKQLWDPGIGQECYDRRREYQLSDSAKYIYLTDIRTAMPSFVPTQDDVLRVRV 180
QY 181 PTTGIIIEYFPDLENIIFRMVDVGQSRERRKWIHCFSVTSIIIFLVALSEYDQVLAECND 240
Db 181 PTTGIIIEYFPDLENIIFRMVDVGQSRERRKWIHCFSVTSIIIFLVALSEYDQVLAECND 240
QY 241 ENRMESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLSIYFPEYTGPKQDVRA 300
Db 241 ENRMESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLSIYFPEYTGPKQDVRA 300
QY 301 ARDFILKLDQDQNPDKREKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 301 ARDFILKLDQDQNPDKREKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
RESULT 4
ABG68591
ID ABG68591 standard; Protein; 353 AA.
XX
AC ABG68591;
XX
DT 07-OCT-2002 (first entry)
XX
DE Mouse G protein alpha sub-unit q family variant #7.
XX
KW G_q protein; sensory signaling; chemoreceptor; tastant; olfactant;
KW pheromone; G protein alpha sub-unit; q family; G alpha q.

XX Mus musculus.
OS
XX
PN WO200236622-A2.
XX
PD 10-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-US32619.
XX
PR 30-OCT-2000; 2000US-243770P.
XX
PA (SENO-) SENOMYX INC.
XX
PI Yao Y, Xu H;
XX
WPI; 2002-519234/55.
XX
PT New G-alpha-q protein variants, useful for analyzing and discovering
PT agonists or antagonists of chemoreceptors, such as G protein coupled
PT receptors involved in sensing of tastants, olfactants or pheromones -
XX
PS Claim 13; Page 25; 32pp; English.
XX
CC The invention describes an isolated variant of a G_q protein, which
CC exhibits increased promiscuity relative to the corresponding G_q protein.
CC The variant is used to identify a compound that modulates sensory
CC signalling in sensory cells and to identify a compound that interacts
CC with the G_q variant protein. The G_q protein variant is useful for
CC analysing and discovering agonists or antagonists of chemoreceptors, such
CC as G protein coupled receptors involved in sensing of tastants,
CC olfactants or pheromones. This is the amino acid sequence of a G protein
CC alpha sub-unit q family (G alpha q) variant that can functionally couple
CC to sensory cell receptors such as taste GPCR's (G protein-coupled
CC receptors) and olfactory GPCR's in an overly promiscuous manner.
XX
SQ Sequence 353 AA;
Query Match 84.1%; Score 1537; DB 23; Length 353;
Best Local Similarity 82.3%; Pred. No. 5.5e-144;
Matches 289; Conservative 34; Mismatches 28; Indels 0; Gaps 0;
QY 5 CCLSAEKESQRTSAEIERHVRDKKARRELKLLLLGTGSGKSTFIKQMRIHSGYS 64
Db 3 CCLSAEKAEARRINDEIERHVRDKKARRELKLLLLGTGSGKSTFIKQMRIHSGYS 62
QY 65 DEDRKGTFLVYQNIIFTAQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 124
Db 63 DEDRKGTFLVYQNIIFTAQAMIRAMDTLKIPIKYEHKNAQAQLVREVDVEKVSADFVDP 122
QY 125 VAAIKQLWDPGIGQECYDRRREYQLSDSAKYIYLTDIRTAMPSFVPTQDDVLRVRVPTTG 184
Db 123 YAAIKSLWDPGIGQECYDRRREYQLSDSTKYIYLNLDLRVADPSYLPQQDDVLRVRVPTTG 182
QY 185 IIEYPEDLENIIFRMVDVGQSRERRKWIHCFSVTSIIIFLVALSEYDQVLAECNDENRM 244
Db 183 IIEYPEDQSVIFRMVDVGQSRERRKWIHCFSVTSIIIFLVALSEYDQVLAECNDENRM 242
QY 245 EESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLSIYFPEYTGPKQDVKAARD 304
Db 243 EESKALFRTIITYPWFONSSVILFNKKDLLEEKIMYSHLVDFPEYDGGPQDQAAREF 302
QY 305 ILKLYQDQNPDKREKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 303 ILKMFVDLNPDSKLIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 353
RESULT 5
ABG68592
ID ABG68592 standard; Protein; 359 AA.
XX
AC ABG68592;
XX
DT 07-OCT-2002 (first entry)

XX DE Mouse G protein alpha sub-unit q family variant #8.
XX AC
KW G,q protein; sensory signaling; chemoreceptor; tastant; olfactant;
KW pheromone; G protein alpha sub-unit; q family; G alpha q.
XX OS
OS Mus musculus.
XX WO200236622-A2.
XX 10-MAY-2002.
XX 24-OCT-2001; 2001WO-US32619.
XX 30-OCT-2000; 2000US-243770P.
XX (SENO-) SENOMYX INC.
XX Yao Y, Xu H;
PI WPI; 2002-519234/55.
XX New G-alpha-q protein variants, useful for analyzing and discovering
PT agonists or antagonists of chemoreceptors, such as G protein coupled
PT receptors involved in sensing of tastants, olfactants or pheromones
XX Claim 13; Page 26; 32pp; English.
XX The invention describes an isolated variant of a G-q protein, which
CC exhibits increased promiscuity relative to the corresponding G-q protein.
CC The variant is used to identify a compound that modulates sensory
CC signaling in sensory cells and to identify a compound that interacts
CC with the G,q variant protein. The G,q protein variant is useful for
CC analysing and discovering agonists or antagonists of chemoreceptors, such
CC as G protein coupled receptors involved in sensing of tastants, such
CC olfactants or pheromones. This is the amino acid sequence of a G protein
CC alpha sub-unit q family (G alpha q) variant that can functionally couple
CC to sensory cell receptors such as taste GPCR's (G protein-coupled
CC receptors) and olfactory GPCR's in an overly promiscuous manner.
XX SQ Sequence 359 AA;

Query Match 84.1%; Score 1537; DB 23; Length 359;
Best Local Similarity 82.3%; Pred. No. 5.6e-144;
Matches 289; Conservative 34; Mismatches 28; Indels 0; Gaps 0;
QY 5 CCLSAEKEKESORISAEIERHVRDCKDARRELKLLLTGSGSKSTFIKQMRIHSGSYS 64
DB 9 CCUSEEAKARRINDEIERHVRDCKDARRELKLLLTGSGSKSTFIKQMRIHSGSYS 68
QY 65 DEDKRGFTKLVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAKIIRREVVDKVTALSRDQ 124
DB 69 DEDKRGFTKLVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAKIIRREVVDKVTALSRDQ 128
QY 125 VAAIKQLWLDPGIOECYDRRREYQLSDSAKYLLTDIERIAMPSEVPTQDDVLRVPTTG 184
DB 129 VAAIKQLWLDPGIOECYDRRREYQLSDSAKYLLTDIERIAMPSEVPTQDDVLRVPTTG 188
QY 185 IIEYFPDLENIIFRMVDVGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECNENRM 244
DB 189 IIEYFPDLSQVIFRMVDVGGORSERRKWIHCFENVTSIMFLVALSEYDQVLAECNENRM 248
QY 245 EESKALFTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISYFPEYTPGPKQDQAARDF 304
DB 249 EESKALFTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISYFPEYTPGPKQDQAARDF 308
QY 305 ILKLYQDQNPDKKVIYSHFTCATDTENIRVFVAAVKDTILQLNLREFNLY 355
DB 309 ILKMFVDLNPDSKIIYSHFTCATDTENIRVFVAAVKDTILQLNLREFNLY 359

RESULT 6
AAM48816

ID AAM48816 standard; Protein; 359 AA.
XX
AC AAM48816;
XX
DT 24-APR-2002 (first entry)
XX
DE Murine G-protein 6q14myr.
XX
KW Mouse; G-protein coupled receptor modulator; G-protein 6q14myr;
KW signal transduction.
XX
OS Mus musculus.
XX WO200204665-A2.
XX 17-JAN-2002.
XX 05-JUL-2001; 2001WO-EP07667.
XX 08-JUL-2000; 2000DE-1033353.
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX Kostenis E;
PI WPI; 2002-148182/19.
XX N-PSDB; ABA97518.
DR
DR
XX
XX
PT Identifying compounds that modify activity of signal transduction
PT pathways, useful potentially as therapeutic agents, by screening with
PT cells that contain hybrid G proteins -
XX
PS Claim 22; Page 24-25; 34pp; German.
XX
CC The present invention relates to a method of identifying compounds which
CC are capable of modifying the activity of a signal transduction pathway
CC which is dependent upon a G-protein coupled receptor. These compounds may
CC include the novel G-proteins 6q14myr (shown here), 6q15myr, 6q14, 6q85
CC and Galphal0.
XX SQ Sequence 359 AA;

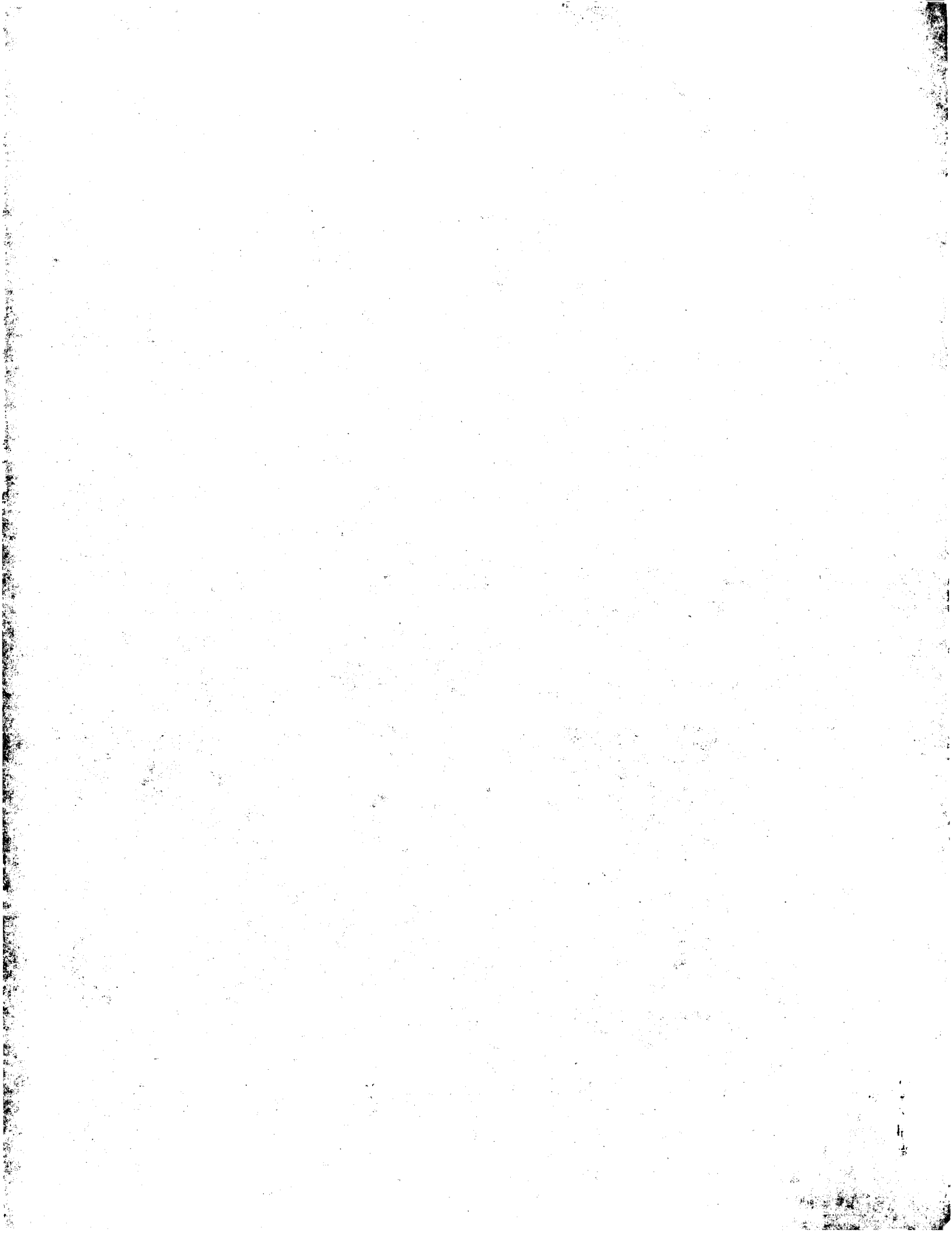
Query Match 84.0%; Score 1535; DB 23; Length 359;
Best Local Similarity 82.1%; Pred. No. 8.9e-144;
Matches 288; Conservative 35; Mismatches 28; Indels 0; Gaps 0;
QY 5 CCLSAEKEKESORISAEIERHVRDCKDARRELKLLLTGSGSKSTFIKQMRIHSGSYS 64
DB 9 CCUSEEAKARRINDEIERHVRDCKDARRELKLLLTGSGSKSTFIKQMRIHSGSYS 68
QY 65 DEDKRGFTKLVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAKIIRREVVDKVTALSRDQ 124
DB 69 DEDKRGFTKLVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAKIIRREVVDKVTALSRDQ 128
QY 125 VAAIKQLWLDPGIOECYDRRREYQLSDSAKYLLTDIERIAMPSEVPTQDDVLRVPTTG 184
DB 129 VAAIKQLWLDPGIOECYDRRREYQLSDSAKYLLTDIERIAMPSEVPTQDDVLRVPTTG 188
QY 185 IIEYFPDLENIIFRMVDVGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECNENRM 244
DB 189 IIEYFPDLSQVIFRMVDVGGORSERRKWIHCFENVTSIMFLVALSEYDQVLAECNENRM 248
QY 245 EESKALFTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISYFPEYTPGPKQDQAARDF 304
DB 249 EESKALFTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISYFPEYTPGPKQDQAARDF 308
QY 305 ILKLYQDQNPDKKVIYSHFTCATDTENIRVFVAAVKDTILQLNLREFNLY 355
DB 309 ILKMFVDLNPDSKIIYSHFTCATDTENIRVFVAAVKDTILQLNLREFNLY 359

RESULT 7
ABG68588

|||||
Db 249 EESKALFRTIITYPWFONSSVILFLNKKDLLEEKIMYSHLVDFPEYDGPQDAQAAREF 308
QY 305 ILKLYQDNPDKEKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 309 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 359
RESULT 9
ABG68585
ID ABG68585 standard; Protein; 353 AA.
XX AC ABG68585;
XX DT 07-OCT-2002 (first entry)
XX DE Mouse G protein alpha sub-unit q family variant #1.
XX KW G-q protein; sensory signaling; chemoreceptor; tastant; olfactant;
XX KW pheromone; G protein alpha sub-unit; q family; G alpha q.
XX OS Mus musculus.
XX PN WO200236622-A2.
XX PD 10-MAY-2002.
XX XX 24-OCT-2001; 2001WO-US32619.
XX PF 30-OCT-2000; 2000US-243770P.
XX PR (SENO-) SENOMYX INC.
XX PA Yao Y, Xu H;
XX PI WPI; 2002-519234/55.
XX DR New G-alpha-q protein variants, useful for analyzing and discovering
XX PT agonists or antagonists of chemoreceptors, such as G protein coupled
XX PT receptors involved in sensing of tastants, olfactants or pheromones
XX PS Claim 13; Page 23; 32pp; English.
XX CC The invention describes an isolated variant of a G-q protein, which
XX CC exhibits increased promiscuity relative to the corresponding G-q protein.
XX CC The variant is used to identify a compound that modulates sensory
XX CC signaling in sensory cells and to identify a compound that interacts
XX CC with the G-q variant protein. The G-q protein variant is useful for
XX CC analysing and discovering agonists or antagonists of chemoreceptors, such
XX CC as G protein coupled receptors involved in sensing of tastants,
XX CC olfactants or pheromones. This is the amino acid sequence of a G protein
XX CC alpha sub-unit q family (G alpha q) variant that can functionally couple
XX CC to sensory cell receptors such as taste GPCR's (G protein-coupled
XX CC receptors) and olfactory GPCR's in an overly promiscuous manner.
XX SQ Sequence 353 AA;
Query Match 83.5%; Score 1527; DB 23; Length 353;
Best Local Similarity 81.8%; Pred. No. 5.4e-143;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;
QY 5 CCLSAEKEESORISAEIERHVRDKDARRELKLLLTGTGSGKSTFTKQMRIHGSYS 64
Db 3 CCLSEAEKARRINDEIERHVRDKDARRELKLLLTGTGSGKSTFTKQMRIHGSYS 62
QY 65 DEDRKGFTKLVYQNTFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTALSRDQ 124
Db 63 DEDRKGFTKLVYQNTFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTALSRDQ 122
QY 125 VAAIKQLWLDPCIOECYDRRREYQLSDSAKYLLTDIERIAMPSPFVPTQDVLVRVPTTG 184
Db 123 VDAIKSLWNDPGIOECYDRRREYQLSDSKYLLNLDLRVADPSYLPQTQDVLVRVPTTG 182

QY 185 IIEYPTDLENIIPRMVDVGQORSERKWIHCFSVTSIIIFLVALSEYDQVLAECNENRM 244
Db 183 IIEYPTDLSVIFRMVDVGQORSERKWIHCFSVTSIIIFLVALSEYDQVLAECNENRM 242
QY 245 EESKALFRTIITYPWFONSSVILFLNKKDLLEEKIMYSHLVDFPEYDGPQDAQAAREF 304
Db 243 EESKALFRTIITYPWFONSSVILFLNKKDLLEEKIMYSHLVDFPEYDGPQDAQAAREF 302
QY 305 ILKLYQDNPDKEKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 303 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 353
RESULT 10
ABG68600
ID ABG68600 standard; Protein; 353 AA.
XX AC ABG68600;
XX DT 07-OCT-2002 (first entry)
XX DE Human G protein alpha sub-unit q family variant #2.
XX KW G-q protein; sensory signaling; chemoreceptor; tastant; olfactant;
XX KW pheromone; G protein alpha sub-unit; q family; G alpha q.
XX OS Homo sapiens.
XX PN WO200236622-A2.
XX PD 10-MAY-2002.
XX PF 24-OCT-2001; 2001WO-US32619.
XX PR 30-OCT-2000; 2000US-243770P.
XX XX (SENO-) SENOMYX INC.
XX PI Yao Y, Xu H;
XX DR WPI; 2002-519234/55.
XX XX New G-alpha-q protein variants, useful for analyzing and discovering
XX PT agonists or antagonists of chemoreceptors, such as G protein coupled
XX PT receptors involved in sensing of tastants, olfactants or pheromones
XX PS Claim 13; Page 29; 32pp; English.
XX CC The invention describes an isolated variant of a G-q protein, which
XX CC exhibits increased promiscuity relative to the corresponding G-q protein.
XX CC The variant is used to identify a compound that modulates sensory
XX CC signaling in sensory cells and to identify a compound that interacts
XX CC with the G-q variant protein. The G-q protein variant is useful for
XX CC analysing and discovering agonists or antagonists of chemoreceptors, such
XX CC as G protein coupled receptors involved in sensing of tastants,
XX CC olfactants or pheromones. This is the amino acid sequence of a G protein
XX CC alpha sub-unit q family (G alpha q) variant that can functionally couple
XX CC to sensory cell receptors such as taste GPCR's (G protein-coupled
XX CC receptors) and olfactory GPCR's in an overly promiscuous manner.
XX SQ Sequence 353 AA;
Query Match 83.5%; Score 1527; DB 23; Length 353;
Best Local Similarity 81.8%; Pred. No. 5.4e-143;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;
QY 5 CCLSAEKEESORISAEIERHVRDKDARRELKLLLTGTGSGKSTFTKQMRIHGSYS 64
Db 3 CCLSEAEKARRINDEIERHVRDKDARRELKLLLTGTGSGKSTFTKQMRIHGSYS 62
QY 65 DEDRKGFTKLVYQNTFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTALSRDQ 124
Db 63 DEDRKGFTKLVYQNTFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTALSRDQ 122

	QY	125	VAAIKQLWLDPGIQECVDRREYQLSDSAKYYLTDIERIAMPSPVPQTQQDVLVRVPTTG	184
	Dd	123	YAAIKSLWNDPGIECVDRRERAYQLSOSTKYLLNDLRVDADPAFLPQTQQDVLRVVPTTG	182
	QY	185	IIEYPFPLENTIFRMWDVGGORSERRKIHCFSVTSTIIPLVALSEXDOYLAECDNENRM	244
	Dd	183	IIEYPDLOQSIVFMWDVGGOSESERRKIHCFFENVTSIMFLVALUSEYDDOVLVESDNENRM	242
	QY	245	EESKALFTTIITYPFNLSSVILFNKKOLLEEKIMYSHLISYPEYTGPQRDVKAARDF	304
	Dd	243	EESKALFTTIITYPFNFONSSVILLFNKKOLLEEKIMYSHLVDYFPDYGGPDQAQAAREF	302
	QY	305	ILKLVDQNPPDKKVITYSHETCATDTENTIRPVFAAVKDITLQLMLRENLY	355
	Dd	303	LKMFEVOLNPDSOKIITYSHETCATDTENTIRVFVAARKDITLQLNLKEYLV	353
	RESULT	11		
	ABG68584	ID	ABG68584 standard; Protein; 359 AA.	
	XX	AC	ABG68584;	
	XX	DT	07-OCT-2002 (first entry)	
	XX	DE	Mouse G protein alpha sub-unit q family.	
	KX	G	G-q protein; sensory signaling; chemoreceptor; tastant; olfactant;	
	KW	p	pheromone; G protein alpha sub-unit; q family; G alpha q.	
	OS	Mus musculus.		
	XX	WO200236622-A2.		
	Pd	10-MAY-2002.		
	XX	24-OCT-2001; 2001WO-US32619.		
	XX	30-OCT-2000; 2000US-243770P.		
	PR	(SENSO-) SENOMYX INC.		
	PI	Yao Y., Xu H.;		
	PS	WIPO; 2002-519234/55.		
	XX	New G-alpha-q protein variants, useful for analyzing and discovering agonists or antagonists of chemoreceptors, such as G protein coupled receptors involved in sensing of tastants, olfactants or pheromones - Claim 13; Fig 1; 32pp; English.		
	CC	The invention describes an isolated variant of a G_q protein, which exhibits increased promiscuity relative to the corresponding G_q protein. The variant is used to identify a compound that modulates sensory signaling in sensory cells and to identify a compound that interacts with the G_q variant protein. The G_q protein variant is useful for analysing and discovering agonists or antagonists of chemoreceptors, such as G protein coupled receptors involved in sensing of tastants, olfactants or pheromones. This is the amino acid sequence of a G protein alpha sub-unit q family (G alpha q) protein that can functionally couple to sensory cell receptors such as taste GPCR's (G protein-coupled receptors) and olfactory GPCR's in an overly promiscuous manner.		
	SQ	Sequence	359 AA;	
	Query Match		83.5%; Score 1527; DB 23; Length 359;	
	Best Local Similarity		81.8%; Pred. No. 5.6e-143;	
	Matches	287; Conservative	35; Mismatches 29; Indels 0; Gaps 0;	
	QY	5	CCLSAEKEKSORTISAETERHVRDKDARRRELKLLLGTGESGSKSTFKQMRIIHSGSYS	64



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OM protein - protein search, using sw model

Run on: February 3, 2003, 14:10:47 ; Search time 16 Seconds
(without alignments)
652.821 Million cell updates/sec

Title: us-09-492-028-2

Perfect score: 1828

Sequence: 1 MAGCCCLSAEKEKESORISAE.....VFAAVKDTILQLNREFNLV 355

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	57.0	374	4	US-09-442-349A-29
2	1042	57.0	374	4	US-09-442-349A-31
3	1041	56.9	374	4	US-09-442-349A-21
4	1041	56.9	374	4	US-09-442-349A-23
5	1041	56.9	374	4	US-09-442-349A-25
6	1041	56.9	374	4	US-09-442-349A-30
7	1041	56.9	374	4	US-09-442-349A-32
8	1041	56.9	374	4	US-09-442-349A-34
9	1040	56.9	374	4	US-09-442-349A-2
10	1040	56.9	374	4	US-09-442-349A-22
11	1040	56.9	374	4	US-09-442-349A-24
12	1040	56.9	374	4	US-09-442-349A-33
13	1037	56.7	374	4	US-09-442-349A-26
14	1037	56.7	374	4	US-09-442-349A-34
15	1036	56.7	374	4	US-09-442-349A-20
16	1036	56.7	374	4	US-09-442-349A-27
17	1022	55.9	374	3	US-08-878-801-4
18	1021	55.9	374	4	US-09-442-349A-14
19	1021	55.9	374	4	US-09-442-349A-16
20	1020	55.8	365	4	US-09-442-349A-108
21	1020	55.8	374	4	US-09-442-349A-6
22	1020	55.8	374	4	US-09-442-349A-8
23	1020	55.8	374	4	US-09-442-349A-10
24	1020	55.8	374	4	US-09-442-349A-15
25	1020	55.8	374	4	US-09-442-349A-17
26	1020	55.8	374	4	US-09-442-349A-19
27	1019	55.7	374	4	US-09-442-349A-1

ALIGNMENTS

RESULT 1

US-09-442-349A-29
; Sequence 29, Application US/09442349A
; Patent No. 6462178

; GENERAL INFORMATION:

; APPLICANT: Wong, Yung H

; TITLE OF INVENTION: G Protein

; FILE REFERENCE: M99/0101/US

; CURRENT APPLICATION NUMBER: US/09/442,349A

; CURRENT FILING DATE: 1999-11-17

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 29

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: G protein

; OTHER INFORMATION: chimera

US-09-442-349A-29

28	1019	55.7	374	4	US-09-442-349A-7	Sequence 7, Appl1
29	1019	55.7	374	4	US-09-442-349A-9	Sequence 9, Appl1
30	1019	55.7	374	4	US-09-442-349A-18	Sequence 18, Appl1
31	1016	55.6	374	4	US-09-442-349A-11	Sequence 11, Appl1
32	1016	55.6	374	4	US-09-442-349A-13	Sequence 13, Appl1
33	1015	55.5	374	4	US-09-442-349A-5	Sequence 5, Appl1
34	1015	55.5	374	4	US-09-442-349A-12	Sequence 12, Appl1
35	1014	55.5	374	4	US-09-442-349A-36	Sequence 36, Appl1
36	1014	55.5	374	4	US-09-442-349A-38	Sequence 38, Appl1
37	1013	55.4	374	3	US-08-878-801-2	Sequence 2, Appl1
38	1013	55.4	374	4	US-09-442-349A-3	Sequence 3, Appl1
39	1013	55.4	374	4	US-09-442-349A-37	Sequence 37, Appl1
40	1013	55.4	374	4	US-09-442-349A-48	Sequence 48, Appl1
41	1013	55.4	374	4	US-09-442-349A-50	Sequence 50, Appl1
42	1013	55.4	374	4	US-09-442-349A-54	Sequence 54, Appl1
43	1013	55.4	374	4	US-09-442-349A-56	Sequence 56, Appl1
44	1013	55.4	374	4	US-09-442-349A-105	Sequence 105, App
45	1012	55.4	374	4	US-09-442-349A-39	Sequence 39, Appl1

Query Match	57.0%	Score 1042	DB 4	Length 374
Best Local Similarity	56.7%	Pred. No. 1.2e-104		
Matches 207	Conservative 56	Mismatches 88	Indels 14	Gaps 3

Qy	4	CC--CLSAEKEKESORISAEIERHVRDKDARRELKLLLTGTGSGKSTFTIKOMRIHGS	61
Db	9	CCPWLTEDEKAAARVDQENRILLEKQKQDQKGLKLLLLGPGSGKSTFTIKOMRIHGA	68
Qy	62	GYSEDEKRGFKLVYQNIFFAMQAMIRAMDTRLTOYCEQNKNAQIIRVEVDKVTALS	121
Db	69	GYSEERKGRPLVYQNIFFVSMRAMIEAMERLQIPFSRPSKHHASLVMSQDPKYKVTTFE	128
Qy	122	RDQVAATKQLWLDPGIOECYDRREYOLSDSAKYVLLTDIERIAMPSPVPTQDDVLRVRP	181
Db	129	KRYAAAWQLMRDAGIRACRYERREFHLLDSAVYTLSHLERITEGYVPTQDDVLRGRMP	188
Qy	182	TTGIIETPFDELNIIFRMVDVGGQSRERRKWIHCFSVTSITIFLVALSEYDOVLAECDNE	241
Db	189	TTGINEYCFVSQKTNLRIVDVGQKSERKWIHCFFENVALIYLASLSEYDOCLEENQOE	248
Qy	242	NRMEESKALPFTITYPWFNLNSVILFLNKKDLLEEKIMYSHLISYPPEYTPGPKQDVKAA	301
Db	249	NRMKESALFCTILELPWFKSTSVILFLNKTDLLEEKIPTSHLATYFPFGPKQDAEAA	308
Qy	302	RDFTLKLY-----QDQNPDKK-KVIYSHFTCATDTENIRFVFAAKVDILQLNL	349
Db	309	KRFILDMYTRMYTCVDPGEGSNRKNKETKIYSHFTCATDTKNIQFVFAVTDIIONNL	368
Qy	350	REFNL 354	

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera
US-09-442-349A-21

Query Match          56.9%; Score 1041; DB 4; Length 374;
Best Local Similarity 56.7%; Pred. No. 1.5e-104;
Matches 207; Conservative 56; Mismatches 88; Indels 14; Gaps 3;

QY 4 CC--CLSAEKEKESQRI  SAEIERHVR  RDKKARRELKLL  LLLGTGSGKSTFI  KOMRIIHGS  61
   ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  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; OTHER INFORMATION: chimera
US-09-442-349A-32

Query Match 56.9%; Score 1041; DB 4; Length 374;
Best Local Similarity 56.7%; Pred. No. 1.5e-104;
Matches 207; Conservative 55; Mismatches 89; Indels 14; Gaps 3;

QY 4 CC--CLSAEKEQSRIASAEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHGS 61
DB 9 CCPWCLTEDEKAAARVDQEIINRILLEQKQDQRGELKLLLLGPGESGSKSTFIKQRIIHA 68

QY 62 GYSDEDRKGFVKLYQNIFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTALS 121
DB 69 GYSEERKGFPLVYQNIFFVSMRAMIEMERLQIPFSRPESKHHASLVMSQDPYKVTTFE 128

QY 122 RDQVAAIKQLWLDPGIOECYDRRREYQSDSAKYILTDIERIAMPSEVPTQODVLRVRVP 181
DB 129 KRYAAAMQWLWRDAGIRACYERREFHLLDSAVYILSHLERITEEGYVPTAQDVLRSMP 188

QY 182 TTGIIYPPFDLENIIFRMVDVGGORSERRKWIHCFSVTSIIFLVALSEYDQVLAECNE 241
DB 189 TTGINEYCFVQKTNLRIVDVGQKSERKKWIHCFFENVIALIYLASLSEYDQCLEENNQE 248

QY 242 NRMEESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYFPETGPKQDVKAA 301
DB 249 NRMEKSLAFCTILELPWFKSTSVILFNKTDILEEKIPTSHLATYFPSPFGPKQDAEAA 308

QY 302 RDFILKLY-----QDQNPDK-KVIYSHFTCATDTENIRFVFAAVKDTILOLNL 349
DB 309 KRFLDMYTRMTGCVDPGEGSNRNKETKEYSHFTCATDTNNIQFVFAVTDVLIQNNL 368

QY 350 REFNL 354
DB 369 KYIGL 373

RESULT 9

US-09-442-349A-2
; Sequence 2, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: Chimera
US-09-442-349A-2

Query Match 56.9%; Score 1040; DB 4; Length 374;
Best Local Similarity 56.7%; Pred. No. 1.9e-104;
Matches 207; Conservative 55; Mismatches 89; Indels 14; Gaps 3;

QY 4 CC--CLSAEKEQSRIASAEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHGS 61
DB 9 CCPWCLTEDEKAAARVDQEIINRILLEQKQDQRGELKLLLLGPGESGSKSTFIKQRIIHA 68

QY 62 GYSDEDRKGFVKLYQNIFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTALS 121
DB 69 GYSEERKGFPLVYQNIFFVSMRAMIEMERLQIPFSRPESKHHASLVMSQDPYKVTTFE 128

QY 122 RDQVAAIKQLWLDPGIOECYDRRREYQSDSAKYILTDIERIAMPSEVPTQODVLRVRVP 181
DB 129 KRYAAAMQWLWRDAGIRACYERREFHLLDSAVYILSHLERITEEGYVPTAQDVLRSMP 188

QY 182 TTGIIYPPFDLENIIFRMVDVGGORSERRKWIHCFSVTSIIFLVALSEYDQVLAECNE 241
DB 189 TTGINEYCFVQKTNLRIVDVGQKSERKKWIHCFFENVIALIYLASLSEYDQCLEENNQE 248

QY 242 NRMEESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYFPETGPKQDVKAA 301
DB 249 NRMEKSLAFCTILELPWFKSTSVILFNKTDILEEKIPTSHLATYFPSPFGPKQDAEAA 308

QY 302 RDFILKLY-----QDQNPDK-KVIYSHFTCATDTENIRFVFAAVKDTILOLNL 349
DB 309 KRFLDMYTRMTGCVDPGEGSNRNKETKEYSHFTCATDTNNIQFVFAVTDVLIQNNL 368

QY 350 REFNL 354
DB 369 KYIGL 373

RESULT 10

US-09-442-349A-22

; Sequence 22, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera
US-09-442-349A-22

Query Match 56.9%; Score 1040; DB 4; Length 374;
Best Local Similarity 56.7%; Pred. No. 1.9e-104;
Matches 207; Conservative 55; Mismatches 89; Indels 14; Gaps 3;

QY 4 CC--CLSAEKEKESORISAEIERHVRDCKDARRELKLLLLGTGSGSKSTFIKQMRIHGS 61
DB 9 CCPWCLTEDEKAAARVDQEIINRILLEQKQDQGEKLLLLGPGSGSKSTFIKQMRIHGA 68
QY 62 GYSDEDRKGTFLVYQNIETAMQAMIRAMDTLRIOYMCEQNKNAQIIRREVVDKVTALS 121
DB 69 GYSEERKGRPLVYQNIETAMQAMIRAMDTLRIOYMCEQNKNAQIIRREVVDKVTALS 128
QY 122 RDQVAAIKQLWLDPGIOECYDRRREYQSDSAKYIYLDIERIAMPSPVPTQDDVLRVRVP 181
DB 129 KRYAAAMQWLWRDAGIRACYERRERFHLSDSAVYLSHLERITEEGYVPTAQDVLRSMP 188
QY 302 RDFILKLY-----QDQNDKE-KVIYSHFTCATDTENIRFVFAAVKDTILQNL 349
DB 309 KRFLDMYTRMYTCVDPGSGNRNKKETKEYSHFTCATDTNNIQFVDAVTDVLIQNNL 368
QY 350 REFNL 354
DB 369 KYIGL 373

RESULT 11
US-09-442-349A-24
; Sequence 24, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera
US-09-442-349A-24

Query Match 56.9%; Score 1040; DB 4; Length 374;
Best Local Similarity 56.7%; Pred. No. 1.9e-104;
Matches 207; Conservative 55; Mismatches 89; Indels 14; Gaps 3;

QY 4 CC--CLSAEKEKESORISAEIERHVRDCKDARRELKLLLLGTGSGSKSTFIKQMRIHGS 61
DB 9 CCPWCLTEDEKAAARVDQEIINRILLEQKQDQGEKLLLLGPGSGSKSTFIKQMRIHGA 68
QY 62 GYSDEDRKGTFLVYQNIETAMQAMIRAMDTLRIOYMCEQNKNAQIIRREVVDKVTALS 121
DB 69 GYSEERKGRPLVYQNIETAMQAMIRAMDTLRIOYMCEQNKNAQIIRREVVDKVTALS 128
QY 122 RDQVAAIKQLWLDPGIOECYDRRREYQSDSAKYIYLDIERIAMPSPVPTQDDVLRVRVP 181
DB 129 KRYAAAMQWLWRDAGIRACYERRERFHLSDSAVYLSHLERITEEGYVPTAQDVLRSMP 188
QY 182 TTGIIIEYPPDLENIIFRMVDVGGGORSRRKWIHCFFESVTSIIFLVALSEYDQVLAECNE 241
DB 189 TTGINCYCFSVQKTNLRIVDVGSGKSRKWIHCFFENVIYLIYLASLSEYDQCLEENNQE 248
QY 242 NRMEESKALFRTIITYPWFNLSSVILFLNKKDLEEKIMYSHLISYFPEYTGPKODVCAA 301
DB 249 NRKESLALFGTILELPWFNSTSVILFNKTDILEEKIPTSHLATYFPGQPKQDAEA 308
QY 302 RDFILKLY-----QDQNDKE-KVIYSHFTCATDTENIRFVFAAVKDTILQNL 349
DB 309 KRFLDMYTRMYTCVDPGSGNRNKKETKEYSHFTCATDTNNIQFVDAVTDVLIQNNL 368
QY 350 REFNL 354
DB 369 KYIGL 373

RESULT 12
US-09-442-349A-33
; Sequence 33, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera
US-09-442-349A-33

Query Match 56.9%; Score 1040; DB 4; Length 374;
Best Local Similarity 56.7%; Pred. No. 1.9e-104;
Matches 207; Conservative 55; Mismatches 89; Indels 14; Gaps 3;

QY 4 CC--CLSAEKEKESORISAEIERHVRDCKDARRELKLLLLGTGSGSKSTFIKQMRIHGS 61
DB 9 CCPWCLTEDEKAAARVDQEIINRILLEQKQDQGEKLLLLGPGSGSKSTFIKQMRIHGA 68
QY 62 GYSDEDRKGTFLVYQNIETAMQAMIRAMDTLRIOYMCEQNKNAQIIRREVVDKVTALS 121
DB 69 GYSEERKGRPLVYQNIETAMQAMIRAMDTLRIOYMCEQNKNAQIIRREVVDKVTALS 128
QY 122 RDQVAAIKQLWLDPGIOECYDRRREYQSDSAKYIYLDIERIAMPSPVPTQDDVLRVRVP 181
DB 129 KRYAAAMQWLWRDAGIRACYERRERFHLSDSAVYLSHLERITEEGYVPTAQDVLRSMP 188
QY 182 TTGIIIEYPPDLENIIFRMVDVGGGORSRRKWIHCFFESVTSIIFLVALSEYDQVLAECNE 241
DB 189 TTGINCYCFSVQKTNLRIVDVGSGKSRKWIHCFFENVIYLIYLASLSEYDQCLEENNQE 248

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OM protein - protein search, using sw model

Run on: February 3, 2003, 14:11:47 ; Search time 13 Seconds
(without alignments)
551.030 Million cell updates/sec

Title: US-09-492-028-2

Perfect score: 1828
Sequence: 1 MAGCCCLSAEKEKSORISAE.....VFAAVKDTILQLNREFNLV 355

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1537	84.1	353	10	US-09-984-292-8
2	1537	84.1	353	10	US-09-989-497-8
3	1537	84.1	359	10	US-09-984-292-9
4	1537	84.1	359	10	US-09-989-497-9
5	1535	84.0	359	10	US-09-899-295-2
6	1530	83.7	359	10	US-09-984-292-11
7	1530	83.7	359	10	US-09-989-497-11
8	1527	83.5	353	10	US-09-984-292-2
9	1527	83.5	353	10	US-09-984-292-17
10	1527	83.5	353	10	US-09-989-497-2
11	1527	83.5	353	10	US-09-989-497-17
12	1527	83.5	359	10	US-09-984-292-1
13	1527	83.5	359	10	US-09-984-292-21
14	1527	83.5	359	10	US-09-989-497-1
15	1527	83.5	359	10	US-09-989-497-21
16	1526	83.5	353	10	US-09-984-292-4
17	1526	83.5	353	10	US-09-984-292-5
18	1526	83.5	353	10	US-09-989-497-4
19	1526	83.5	353	10	US-09-989-497-5

ALIGNMENTS

RESULT 1

US-09-984-292-8
; Sequence 8, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-O PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CURRENT APPLICATION NUMBER: 60/243,770
; FILE REFERENCE: 078003-0280649
; CURRENT FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 353
; ORGANISM: Mus sp.
US-09-984-292-8

Query Match	84.1%	Score	1537	DB	10	Length	353
Best Local Similarity	82.3%	Pred. No.	2e+131				
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Db	3	CCLSAEKARRINDEIRHVRRDKRDARRELKLLLLGTGSGSKSTFIKQMRIHSGYS	62				
Qy	65	DEDRKGTFLKYONFTAMQAMIRAMDTLRTOYCEONKENAQIIREVEVDKVTALS RDQ	124				
Db	63	DEDRKGTFLKYONFTAMQAMIRAMDTLRTOYCEONKENAQIIREVEVDKVTALS RDQ	122				
Qy	125	VAAIKLWLDPGIOECYDRRREYQOLSADAKYLLTDIERIAMPSEVPTQDDVLRVRVPTTG	184				
Db	123	VAAIKLWLDPGIOECYDRRREYQOLSADAKYLLTDIERIAMPSEVPTQDDVLRVRVPTTG	182				
Qy	185	IIIEYPPDLNIIIFRMVDVGQSRERRKWIHCFSVTSIIIFLVALSEYDQVLAECDENRM	244				
Db	183	IIIEYPPDLNIIIFRMVDVGQSRERRKWIHCFSVTSIIIFLVALSEYDQVLAECDENRM	242				


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; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-989-497-2

Query Match      83.5%; Score 1527; DB 10; Length 353;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

QY 5 CCLSAEKEQSRIETAEIERHVRDKKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 64
Db 3 CCLSEAEKARRINDEIERHVRDKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 62
QY 65 DEDRKGTFLVYQNIIFTAMQAMIRAMDTLRIOYMCENKNAQIIRVEVDKVTALSRDQ 124
Db 63 DEDKRGFTKLVIYQNIIFTAMQAMIRAMDTLRIOYMCENKNAQIIRVEVDKVTALSRDQ 122
QY 125 VAAIKQLWLDPGIQECYDRRREYQLSDSAKYIYLTDIRIAMPSFVPTQDDVLRVRVPTTG 184
Db 123 VAAIKSLWNDPGIQECYDRRREYQLSDSTKYIYLNLDLRVADPAYLPQQDDVLRVRVPTTG 182
QY 185 IIEYPPDLENIIFRMVDVGGQSRERRKWIHCFFESVTSIIFLVALSEYDQVLAECNDENRM 244
Db 183 IIEYPPDLQSVIFRMVDVGGQSRERRKWIHCFFENVTSIMELVALSEYDQVLAECNDENRM 242
QY 245 EESKALERTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYPPETGPKQDVKAARDP 304
Db 243 EESKALERTIITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQORDAQAREF 302
QY 305 ILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
Db 303 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 353

RESULT 11
US-09-989-497-17
; Sequence 17, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-497-17

Query Match      83.5%; Score 1527; DB 10; Length 353;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

QY 5 CCLSAEKEQSRIETAEIERHVRDKKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 64
Db 3 CCLSEAEKARRINDEIERHVRDKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 62
QY 65 DEDRKGTFLVYQNIIFTAMQAMIRAMDTLRIOYMCENKNAQIIRVEVDKVTALSRDQ 124
Db 63 DEDKRGFTKLVIYQNIIFTAMQAMIRAMDTLRIOYMCENKNAQIIRVEVDKVTALSRDQ 122
QY 125 VAAIKQLWLDPGIQECYDRRREYQLSDSAKYIYLTDIRIAMPSFVPTQDDVLRVRVPTTG 184
Db 123 VAAIKSLWNDPGIQECYDRRREYQLSDSTKYIYLNLDLRVADPAYLPQQDDVLRVRVPTTG 182
QY 185 IIEYPPDLENIIFRMVDVGGQSRERRKWIHCFFESVTSIIFLVALSEYDQVLAECNDENRM 244
Db 183 IIEYPPDLQSVIFRMVDVGGQSRERRKWIHCFFENVTSIMELVALSEYDQVLAECNDENRM 242
QY 245 EESKALERTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYPPETGPKQDVKAARDP 304
Db 243 EESKALERTIITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQORDAQAREF 302
QY 305 ILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
Db 303 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 353

RESULT 11
US-09-989-497-17
; Sequence 17, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-497-17

Query Match      83.5%; Score 1527; DB 10; Length 353;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;
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QY 5 CCLSAEKEQSRIETAEIERHVRDKKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 64
Db 3 CCLSEAEKARRINDEIERHVRDKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 62
QY 65 DEDRKGTFLVYQNIIFTAMQAMIRAMDTLRIOYMCENKNAQIIRVEVDKVTALSRDQ 124
Db 63 DEDKRGFTKLVIYQNIIFTAMQAMIRAMDTLRIOYMCENKNAQIIRVEVDKVTALSRDQ 122
QY 125 VAAIKQLWLDPGIQECYDRRREYQLSDSAKYIYLTDIRIAMPSFVPTQDDVLRVRVPTTG 184
Db 123 VAAIKSLWNDPGIQECYDRRREYQLSDSTKYIYLNLDLRVADPAYLPQQDDVLRVRVPTTG 182
QY 185 IIEYPPDLENIIFRMVDVGGQSRERRKWIHCFFESVTSIIFLVALSEYDQVLAECNDENRM 244
Db 183 IIEYPPDLQSVIFRMVDVGGQSRERRKWIHCFFENVTSIMELVALSEYDQVLAECNDENRM 242
QY 245 EESKALERTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYPPETGPKQDVKAARDP 304
Db 243 EESKALERTIITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQORDAQAREF 302
QY 305 ILKLYQDQNPDKKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
Db 303 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 353

RESULT 12
US-09-984-292-1
; Sequence 1, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-984-292-1

Query Match      83.5%; Score 1527; DB 10; Length 359;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

QY 5 CCLSAEKEQSRIETAEIERHVRDKKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 64
Db 9 CCLSEAEKARRINDEIERHVRDKRDARRELKLLLLGTGSGKSTFIKQMRIHSGYS 68
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Db 129 VDAIKSLWNDPGIQECYDRRREYQLSDSTKYIYLNLDLRVADPAYLPQQDDVLRVRVPTTG 188
QY 185 IIEYPPDLENIIFRMVDVGGQSRERRKWIHCFFESVTSIIFLVALSEYDQVLAECNDENRM 244
Db 189 IIEYPPDLQSVIFRMVDVGGQSRERRKWIHCFFENVTSIMELVALSEYDQVLAECNDENRM 248
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Db 309 ILKMFVDLPDSDKIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 359
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RESULT 13

US-09-984-292-21
; Sequence 21, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-292-21

Query Match 83.5%; Score 1527; DB 10; Length 359;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

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Db 9 CCLSEAKEARRINDEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHSGYS 68
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 65 DEDRKGFTKLVYQNIETAMQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 124
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Db 69 DEDRKGFTKLVYQNIETAMQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 128
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 125 VAAIKQLWLDPGIOECYDRREYQLSDTSKYLLNDLRVADPVPYLTQQDVLVRVPTTG 184
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Db 129 VAAIKSLWLDPGIOECYDRREYQLSDTSKYLLNDLRVADPVPYLTQQDVLVRVPTTG 188
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 185 IIEYFPDLNIIFRMVDVGGORERRKWIHCFESVTSIIIFLVALSEYDQVLAECNENRM 244
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 189 IIEYFPDLQSVIFRMVDVGGORERRKWIHCFENVTISIMFLVALSEYDQVLAECNENRM 248
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 245 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLISYPEYTPGKQDVKAARD 304
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Db 249 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLISYPEYTPGKQDVKAARD 308
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Qy 305 ILKLYQDNQDPKEKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
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Db 309 ILKMFVDLPDSDKIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 359
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RESULT 14

US-09-989-497-1
; Sequence 1, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-29
; PRIOR FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-989-497-1

Query Match 83.5%; Score 1527; DB 10; Length 359;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

Qy 5 CCLSAEKEKESORISAEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHSGYS 64
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 9 CCLSEAKEARRINDEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHSGYS 68
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 65 DEDRKGFTKLVYQNIETAMQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 124
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 69 DEDRKGFTKLVYQNIETAMQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 128
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 125 VAAIKQLWLDPGIOECYDRREYQLSDTSKYLLNDLRVADPVPYLTQQDVLVRVPTTG 184
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 129 VDAIKSLWLDPGIOECYDRREYQLSDTSKYLLNDLRVADPVPYLTQQDVLVRVPTTG 188
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 185 IIEYFPDLNIIFRMVDVGGORERRKWIHCFESVTSIIIFLVALSEYDQVLAECNENRM 244
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 189 IIEYFPDLQSVIFRMVDVGGORERRKWIHCFENVTISIMFLVALSEYDQVLAECNENRM 248
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 245 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLISYPEYTPGKQDVKAARD 304
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 249 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLISYPEYTPGKQDVKAARD 308
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 305 ILKLYQDNQDPKEKVIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 309 ILKMFVDLPDSDKIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 359
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||

RESULT 15

US-09-989-497-21
; Sequence 21, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-29
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-497-21

Query Match 83.5%; Score 1527; DB 10; Length 359;
Best Local Similarity 81.8%; Pred. No. 1.6e-130;
Matches 287; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

Qy 5 CCLSAEKEKESORISAEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHSGYS 64
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 9 CCLSEAKEARRINDEIERHVRDKDARRELKLLLLGTGSGSKSTFIKQMRIHSGYS 68
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Qy 65 DEDRKGFTKLVYQNIETAMQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 124
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||
Db 69 DEDRKGFTKLVYQNIETAMQAMIRAMDTLRIQYMCENKNAQIIREVEVDKVTALSRDQ 128
||||:| ||| :|:|||||||||||||||||||||||||||||||||:|:||||


```
Qy 125 VAAIKQLWLDPGIQECYDRREYQLSDSAKYIYLDIERIAMPSEVPTQQDVLVRVPTTG 184
    ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 YAAIKSLWNDPGIQECYDRREYQLSDSTKYIYLNLDLDRVADPAYLPTQQDVLVRVPTTG 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 185 IIEYPFDLENIIFRMVDVGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECNENRM 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 IIEYPFDLQSVIFRMVDVGGORSERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRM 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 245 EESKALFRTIITYPWFLNSSVILFLNKKDLLEEKIMYSHLISYFPEYTGPKQDVKAARDF 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 EESKALFRTIITYPWFFONSSVILFLNKKDLLEEKIMYSHLVDPPEYDGGPORDAQAAAREF 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 305 ILKLYQONPDKEKYIYSHFTCATDTENIRFVFAAVKDTILQLNLREFNLV 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 ILKMFVDLNPDSDKIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: February 3, 2003, 14:15:53
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 3, 2003, 14:08:56 ; Search time 13 seconds
(without alignments)
1132.623 Million cell updates/sec

Title: US-09-492-028-2

Perfect score: 1828

Sequence: 1 MAGCCCLSAEKEKSRISAE.....VFAAVKDTILQLNLRNFLV 355

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1828	100.0	355	1 GB14_MOUSE	P30677 mus musculus
2	1780	97.4	355	1 GB14_BOVIN	P38408 bos taurus
3	1771	96.9	355	1 GB14_HUMAN	O95837 homo sapien
4	1643.5	89.9	354	1 GB14_XENLA	P71819 xenopus lae
5	1538	84.1	353	1 GB0_MOUSE	P21279 mus musculus
6	1527	83.5	359	1 GB11_MELGA	P45645 meleagris g
7	1526	83.5	353	1 GB0_RAT	P82471 rattus norv
8	1524	83.4	353	1 GB0_CANFA	Q28294 canis famli
9	1524	83.4	359	1 GB11_HUMAN	P29992 homo sapien
10	1519	83.1	353	1 GB0_HUMAN	P50148 homo sapien
11	1518	83.0	359	1 GB11_BOVIN	P38409 bos taurus
12	1517	83.0	359	1 GB11_XENLA	P43444 xenopus lae
13	1512	82.7	359	1 GB11_MOUSE	P21278 mus musculus
14	1510	82.6	359	1 GB11_RAT	Q91id2 rattus norv
15	1492	81.6	353	1 GB0_XENLA	P38410 xenopus lae
16	1416	77.5	353	1 GB0_PATYE	O15975 patinopecte
17	1407	77.0	353	1 GB0_HOMAM	P91950 homarus ame
18	1406	76.9	353	1 GB0_LYMST	P38411 lymnaea sta
19	1382.5	75.6	354	1 GB0_LOLFO	P38412 loligo forb
20	1346	73.6	353	1 GB0_DROME	P23625 drosophila
21	1022	55.9	374	1 GB15_MOUSE	P30678 mus musculus
22	1013	55.4	374	1 GB15_HUMAN	P30679 homo sapien
23	1002	54.8	374	1 GB15_RAT	O98302 rattus norv
24	910.5	49.8	353	1 GB02_HUMAN	P29777 homo sapien
25	905.5	49.5	353	1 GB02_CRILLO	P17806 cricetus
26	900.5	49.3	353	1 GB0_XENLA	P10825 xenopus lae
27	899.5	49.2	353	1 GB02_MOUSE	P18873 mus musculus
28	899.5	49.2	353	1 GB0_LYMST	P30683 lymnaea sta
29	898.5	49.2	353	1 GB0_HELTI	P51877 helisoma tr
30	895.5	49.0	354	1 GB01_DROME	P16378 drosophila
31	895	49.0	354	1 GB12_CHICK	P50147 gallus gall
32	894.5	48.9	353	1 GB02_RAT	P30033 rattus norv
33	894	48.9	354	1 GB12_RAT	P04897 rattus norv

RESULT 1

ID	GB14_MOUSE	STANDARD	PRT	355 AA
DT	P30677;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Guanine nucleotide-binding protein, alpha-14 subunit.			
GN	GNA14 OR GNA-14.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92052208; PubMed=1946421;			
RA	Wilkie T.M., Scherle P.A., Strathmann M.P., Slepak V.Z., Simon M.I.;			
RT	"Characterization of G-protein alpha subunits in the Gq class:			
RT	expression in murine tissues and in stromal and hematopoietic cell			
RT	lines."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:10049-10053(1991).			
RP	[2]			
RX	SEQUENCE OF 217-267 FROM N.A.			
RA	MEDLINE=90017488; PubMed=2508088;			
RT	Strathmann M., Wilkie T.M., Simon M.I.;			
RT	"Diversity of the G-protein family: sequences from five additional			
RL	alpha subunits in the mouse."			
CC	Proc. Natl. Acad. Sci. U.S.A. 86:7407-7409(1989).			
CC	-!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE			
CC	INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE			
CC	SIGNALING SYSTEMS.			
CC	-!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).			
CC	THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.			
CC	-!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY SUBFAMILY 3 (G(O)).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M80631; AAA83222.1; -			
DR	EMBL; M57616; AAA63304.1; -			
DR	PIR; A41534; A41534.			
DR	PIR; E33833; E33833.			
DR	HSSP; P10824; IBOF.			
DR	MGP; MGI:95769; Gnal4.			
DR	InterPro; IPR001019; Gproteins_alpha.			
DR	Pfam; PF00503; G-alpha; 1.			
DR	PRINTS; PR00318; GPROTEIN.			
DR	ProDom; PD000281; Gprotein_alpha; 1.			
DR	SMART; SM00275; G-alpha; 1.			
KW	GTP-binding; Transducer; Multigene family; ADP-ribosylation.			
FT	NP_BIND 42 49			
	GTP (BY SIMILARITY).			

ALIGNMENTS

34	893	48.9	354	1	GB12_CANFA	P38400 canis famli
35	893	48.9	354	1	GB12_MOUSE	P08752 mus musculu
36	892.5	48.8	353	1	GB11_HUMAN	P04898 homo sapien
37	892.5	48.8	353	1	GB1_ASTPE	P30676 asterina pe
38	891.5	48.8	353	1	GB11_RAT	P10824 rattus norv
39	891	48.7	354	1	GB12_HUMAN	P04899 homo sapien
40	891	48.7	354	1	GB12_ORYLA	O13055 oryzias lat
41	890.5	48.7	353	1	GB11_CHICK	P50146 gallus gall
42	889.5	48.7	353	1	GB11_CAVPO	P38401 cavia porce
43	889	48.6	354	1	GB12_CAVPO	P38402 cavia porce
44	888	48.6	356	1	GB0_PATYE	O15976 patinopecte
45	884.5	48.4	353	1	GB11_XENLA	P27044 xenopus lae

```
FT NP_BIND 201 205 GTP (BY SIMILARITY).
FT NP_BIND 270 273 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT MOD_RES 179 179 (BY SIMILARITY).
SQ SEQUENCE 355 AA; 41522 MW; A4810D72169878E9 CRC64;

Query Match 100.0%; Score 1828; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 6.5e-130;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGCCCLSAEKEQSRIASIERHVRDKKARRELKLLLTGSGSKSTFIKOMRIIHG 60
Db 1 MAGCCCLSAEKEQSRIASIERHVRDKKARRELKLLLTGSGSKSTFIKOMRIIHG 60

QY 61 SGYSDEDRKFTKLIVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAQIIEVEVDKVTAL 120
Db 61 SGYSDEDRKFTKLIVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAQIIEVEVDKVTAL 120

QY 121 SRDQVAIAIKQLWDPGTOECYDRRREYQSDSAKYIYLTDIRIAMPFSFVPTQDVLVRV 180
Db 121 SRDQVAIAIKQLWDPGTOECYDRRREYQSDSAKYIYLTDIRIAMPFSFVPTQDVLVRV 180

QY 181 PTTGIIEYFPDLENIIFRMVDVGQSRERRKWHCFESVTSIIFLVALSEYDQVLAECN 240
Db 181 PTTGIIEYFPDLENIIFRMVDVGQSRERRKWHCFESVTSIIFLVALSEYDQVLAECN 240

QY 241 ENRMESKALFRTIITYPWLNSVILFLNKKDLLEKIMYSHLISYFPEYTGPKQDVKA 300
Db 241 ENRMESKALFRTIITYPWLNSVILFLNKKDLLEKIMYSHLISYFPEYTGPKQDVKA 300

QY 301 ARDFILKLYQDQNDPKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 301 ARDFILKLYQDQNDPKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355

RESULT 2
GB14_BOVIN STANDARD; PRT; 355 AA.
AC P38408;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein, alpha-14 subunit (GL1).
GN GNA14.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91286303; PubMed=1905731;
RA Nakamura F., Ogata K., Shiozaki K., Kameyama K., Ohara K., Haga T.,
RA Nukada T.;
RT Identification of two novel GTP-binding protein alpha-subunits that
RT lack apparent ADP-ribosylation sites for pertussis toxin.";
RL J. Biol. Chem. 266:12676-12681(1991).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(O)).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90335; BAA14349.1; -.
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DR PIR; A40891; A40891.
DR HSSP; P10824; IBOF.
DR InterPro; IP001019; Gprotein_alpha.
DR Pfam; PF0503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
KW GTP-binding; Transducer; Multigene family; ADP-ribosylation.
FT NP_BIND 42 49 GTP (BY SIMILARITY).
FT NP_BIND 201 205 GTP (BY SIMILARITY).
FT NP_BIND 270 273 GTP (BY SIMILARITY).
FT MOD_RES 179 179 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT (BY SIMILARITY).
SQ SEQUENCE 355 AA; 41498 MW; 60888CC6C9B7243B CRC64;

Query Match 97.4%; Score 1780; DB 1; Length 355;
Best Local Similarity 96.6%; Pred. No. 2.6e-126;
Matches 343; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAGCCCLSAEKEQSRIASIERHVRDKKARRELKLLLTGSGSKSTFIKOMRIIHG 60
Db 1 MAGCCCLSAEKEQSRIASIERHVRDKKARRELKLLLTGSGSKSTFIKOMRIIHG 60

QY 61 SGYSDEDRKFTKLIVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAQIIEVEVDKVTAL 120
Db 61 SGYSDEDRKFTKLIVYQNIPTAMQAMIRAMDTLRIQYMCQNKENAQIIEVEVDKVTAL 120

QY 121 SRDQVAIAIKQLWDPGTOECYDRRREYQSDSAKYIYLTDIRIAMPFSFVPTQDVLVRV 180
Db 121 SRDQVAIAIKQLWDPGTOECYDRRREYQSDSAKYIYLTDIRIAMPFSFVPTQDVLVRV 180

QY 181 PTTGIIEYFPDLENIIFRMVDVGQSRERRKWHCFESVTSIIFLVALSEYDQVLAECN 240
Db 181 PTTGIIEYFPDLENIIFRMVDVGQSRERRKWHCFESVTSIIFLVALSEYDQVLAECN 240

QY 241 ENRMESKALFRTIITYPWLNSVILFLNKKDLLEKIMYSHLISYFPEYTGPKQDVKA 300
Db 241 ENRMESKALFRTIITYPWLNSVILFLNKKDLLEKIMYSHLISYFPEYTGPKQDVKA 300

QY 301 ARDFILKLYQDQNDPKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 301 ARDFILKLYQDQNDPKKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355

RESULT 3
GB14_HUMAN STANDARD; PRT; 355 AA.
AC O95837;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein, alpha-14 subunit (G-protein alpha
DE subunit 14).
GN GNA14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99208664; PubMed=10191087;
RA Rubio J.P., Levy E.R., Dobson-Stone C., Monaco A.P.;
RT "Genomic organization of the human G-alpha-14 and G-alpha-Q genes and
RT mutation analysis in chorea-acanthocytosis (CHAC).";
RL Genomics 57:84-93(1999).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(O)).
CC
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CC -----

CC EMBL; AF105201; AADI7944.1; -
CC HSSP; P10824; 1BOF.
CC Genew; HGNC:4382; GNA14.
CC MIM; 604397; -
CC InterPro; IPR001019; Gprotein_alpha.
CC Pfam; PF00503; G-alpha; 1.
CC PRINTS; PR00318; GPROTEIN.
CC ProDom; PD000281; Gprotein_alpha; 1.
CC SMART; SM00275; G-alpha; 1.
CC GTP-binding; Transducer; Multigene family; ADP-ribosylation.
KW NP_BIND 42 49 GTP (BY SIMILARITY).
FT NP_BIND 201 205 GTP (BY SIMILARITY).
FT NP_BIND 270 273 GTP (BY SIMILARITY).
FT MOD_RES 179 179 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT (BY SIMILARITY).
SQ SEQUENCE 355 AA; 41570 MW; EAB73A9876E9C47E CRC64;

Query Match 96.9%; Score 1771; DB 1; Length 355;
Best Local Similarity 96.3%; Pred. No. 1.2e-125;
Matches 342; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAGCCCLSAEKESSQISAEIERHVRDKDARRELKLLLLGTGSGKSTFIKQMRIHG 60
Db 1 MAGCCCLSAEKESSQISAEIERHVRDKDARRELKLLLLGTGSGKSTFIKQMRIHG 60
Qy 61 SGYSDERKGFVKLYQNIPTAMQAMIRAMDTLRIOYVCEONKNAQIIRVEVDKVTAL 120
Db 61 SGYSDERKGFVKLYQNIPTAMQAMIRAMDTLRIOYVCEONKNAQIIRVEVDKVSML 120
Qy 121 SRDQVAATKQLWDPGIEQYDRREYQLSDSAKYLLTDIERIAMPSPVPTQDDVLRVRV 180
Db 121 SREQVEAIKQLWDPGIEQYDRREYQLSDSAKYLLTDIERIATPSPVPTQDDVLRVRV 180
Qy 181 PTTGIIIEYFPDLENIIFRMVDVGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECN 240
Db 181 PTTGIIIEYFPDLENIIFRMVDVGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECN 240
Qy 241 ENRMEESKALFRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYFPEYTGPKQDVKA 300
Db 241 ENRMEESKALFRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYFPEYTGPKQDVRA 300
Qy 301 ARDFILKLYQDQNPDKERKVIYSHFTCATDTENIRFVFAAVKDTIILQLNREFNLV 355
Db 301 ARDFILKLYQDQNPDKERKVIYSHFTCATDTENIRFVFAAVKDTIILQLNREFNLV 355

RESULT 4
ID GB14_XENLA STANDARD; PRT; 354 AA.
AC 073819;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein, alpha-14 subunit.
GN GNA14.

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98344029; PubMed=9677362;
RA Shapira H., Amit I., Revach M., Oron Y., Battey J.F.;
RT "Galphal4 and Galphaq mediate the response to trypsin in Xenopus oocytes.";

RL J. Biol. Chem. 273:19431-19436(1998).
CC -|- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C.
CC MEDIATES RESPONSES TO TRYPSIN.
CC -|- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -|- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (C(O)).
CC -----

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CC -----

CC EMBL; AF059182; AAC41382.1; -
CC HSSP; P10824; 1BOF.
CC InterPro; IPR001019; Gprotein_alpha.
CC Pfam; PF00503; G-alpha; 1.
CC PRINTS; PR00318; GPROTEIN.
CC ProDom; PD000281; Gprotein_alpha; 1.
CC SMART; SM00275; G-alpha; 1.
CC GTP-binding; Transducer; Multigene family; ADP-ribosylation.
KW NP_BIND 41 48 GTP (BY SIMILARITY).
FT NP_BIND 200 204 GTP (BY SIMILARITY).
FT NP_BIND 269 272 GTP (BY SIMILARITY).
FT MOD_RES 178 178 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT (BY SIMILARITY).
SQ SEQUENCE 354 AA; 41595 MW; C7105026B037600E CRC64;

Query Match 89.9%; Score 1643.5; DB 1; Length 354;
Best Local Similarity 89.3%; Pred. No. 4.3e-116;
Matches 317; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MAGCCCLSAEKESSQISAEIERHVRDKDARRELKLLLLGTGSGKSTFIKQMRIHG 60
Db 1 MAGCCCLSAEKESSQISAEIERHVRDKDARRELKLLLLGTGSGKSTFIKQMRIHG 59
Qy 61 SGYSDERKGFVKLYQNIPTAMQAMIRAMDTLRIOYVCEONKNAQIIRVEVDKVTAL 120
Db 60 SYTDEDKRGFTKLYQNIPTSMQSMIRAMDTLRIOYVCEONKNAQIIRVEVDKVSLL 119
Qy 121 SRDQVAATKQLWDPGIEQYDRREYQLSDSAKYLLTDIERIAMPSPVPTQDDVLRVRV 180
Db 120 ERKHVEAIKQLWDPGIEQYDRREYQLSDSAKYLLTDIERIAMPSPVPTQDDVLRVRV 179
Qy 181 PTTGIIIEYFPDLENIIFRMVDVGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECN 240
Db 180 PTTGIIIEYFPDLENIIFRMVDVGGORSERRKWIHCFENVTIIFLVALSEYDQVLAECN 239
Qy 241 ENRMEESKALFRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYFPEYTGPKQDVKA 300
Db 240 ENRMEESKALFRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLIDYFPFPGKQDSOA 299
Qy 301 ARDFILKLYQDQNPDKERKVIYSHFTCATDTENIRFVFAAVKDTIILQLNREFNLV 355
Db 300 ARDFILKLYQDQNPDKERKVIYSHFTCATDTENIRFVFAAVKDTIILQLNREFNLV 354

RESULT 5
ID GBQ_MOUSE STANDARD; PRT; 353 AA.
AC P21279;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein G(q), alpha subunit.
GN GNAQ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.


```
Db 129 VSAIRTLWDPGICQYDRRREYQLSDSAKYVLSVDRIATPGYLTQODVLVRVPTTG 188
Qy 185 IIEYFDLENIIFRMVDVGGQSRKKWTHCFESVTSIIFLValseyDOVLAECNENRM 244
Db 189 IIEYFDLENIIFRMVDVGGQSRKKWTHCFENVTSMFLValseyDOVLAECNENRM 248
Qy 245 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLSYFFPEYTGPKODVKAARDF 304
Db 249 EESKALFTIITYPWFQNSVILFLNKKDLLEEDKILYSHLVDFPEFDGPDQDAQAAREF 308
Qy 305 ILKLYQDQNPQKEVIYSHFTCATDTENIRFVFAAVKDTIQLNLREFNLV 355
Db 309 ILKMEVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTIQLNLKEYNLV 359

RESULT 7
GBQ_RAT
ID GBQ_RAT STANDARD: PRT; 353 AA.
AC P82471;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Guanine nucleotide-binding protein G(q), alpha subunit.
GN GNAQ.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strotmann R.;
RT "Rat G alpha q subunit.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 74-229 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=93081611; PubMed=1333286;
RA Lesch K.-P., Manji H.K.;
RT "Signal-transducing G proteins and antidepressant drugs: evidence for
modulation of alpha subunit gene expression in rat brain.";
RL Biol. Psychiatry 32:549-579(1992).
RN [3]
RP SEQUENCE OF 238-331 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney cortex;
RA Thomas C.P.;
RT "GTP-binding protein expression in glomerular mesangial cells.";
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
-----
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-----
DR EMBL; AF234260; AAF59930.1; ALT_INIT.
DR EMBL; L37294; AAB02848.1; -.
DR HSSP; P10824; IBOF.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
KW GTP-binding; Transducer; Multigene family; ADP-ribosylation;
KW Palmitate; Lipoprotein.
FT LIPID 3 PALMITATE (BY SIMILARITY).
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FT LIPID 4 4 PALMITATE (BY SIMILARITY).
FT NP_BIND 40 47 GTP (BY SIMILARITY).
FT NP_BIND 199 203 GTP (BY SIMILARITY).
FT NP_BIND 268 271 GTP (BY SIMILARITY).
FT MOD_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT (BY SIMILARITY).
FT CONFLICT 85 85 V -> I (IN REF. 2).
SQ SEQUENCE 353 AA; 41469 MW; BB4C211FDDDA7534 CRC64;

Query Match 83.5%; Score 1526; DB 1; Length 353;
Best Local Similarity 81.5%; Pred. No. 2.7e-107;
Matches 286; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

Qy 5 CCLSAEKEESORISAEIERHVRDKKARRELKLLLLGTGSGKSTFIKQRIIHSGYS 64
Db 3 CCLSEAEARRINDEIERQLRRDKARRELKLLLLGTGSGKSTFIKQRIIHSGYS 62
Qy 65 DEDRGFTKLVYONIFTAMQAMIRAMDTLRIQYMCQNKENAIQIREVEVDKVTALSRDQ 124
Db 63 DEDKRGFTKLVYONIFTAMQAMVRAMDTLKIPYKYEHNKAHAQLVREVDVKVSAPENY 122
Qy 125 VAAIKQLKLDPGIOECYDRRREYQLSDSAKYVLSVDRIATPGYLTQODVLVRVPTTG 184
Db 123 VDAIKSLANDPGIOECYDRRREYQLSDSTKYVLSVDRIATPGYLTQODVLVRVPTTG 182
Qy 185 IIEYFDLENIIFRMVDVGGQSRKKWTHCFESVTSIIFLValseyDOVLAECNENRM 244
Db 183 IIEYFDLQSVIFRMVDVGGQSRKKWTHCFENVTSMFLValseyDOVLAECNENRM 242
Qy 245 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLSYFFPEYTGPKODVKAARDF 304
Db 243 EESKALFTIITYPWFQNSVILFLNKKDLLEEKIMYSHLVDFPEYDGPDQDAQAAREF 302
Qy 305 ILKLYQDQNPQKEVIYSHFTCATDTENIRFVFAAVKDTIQLNLREFNLV 355
Db 303 ILKMEVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTIQLNLKEYNLV 353

RESULT 8
GBQ_CANFA
ID GBQ_CANFA STANDARD: PRT; 353 AA.
AC Q28294;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein G(q), alpha subunit.
GN GNAQ.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96433124; PubMed=8836152;
RA Johnson G.J., Lels L.A., Dunlop P.C.;
RT "Specificity of G alpha q and G alpha 11 gene expression in platelets
and erythrocytes. Expressions of cellular differentiation and species
differences.";
RL Biochem. J. 318:1023-1031(1996).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
-----
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CC -----
DR EMBL; L76257; AAB05348.1; ALT_INIT.
DR HSSP; P10824; 1BOF.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
KW GTP-binding; Transducer; Multigene family; ADP-ribosylation;
KW Palmitate; Lipoprotein.
FT LIPID 3 3 PALMITATE (BY SIMILARITY).
FT LIPID 4 4 PALMITATE (BY SIMILARITY).
FT NP_BIND 40 47 GTP (BY SIMILARITY).
FT NP_BIND 199 203 GTP (BY SIMILARITY).
FT NP_BIND 268 271 GTP (BY SIMILARITY).
FT MOD_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT MOD_RES 177 177 (BY SIMILARITY).
SQ SEQUENCE 353 AA; 41467 MW; E7737E07B1F4904C CRC64;
Query Match 83.4%; Score 1524; DB 1; Length 353;
Best Local Similarity 81.5%; Pred. No. 3.8e-107;
Matches 286; Conservative 36; Mismatches 29; Indels 0; Gaps 0;
QY 5 CCLSAEKEKESQISAEIERHVRDCKDARRELKLLLTGTGSGKSTFIKQMRIHSGYS 64
DB 3 CCLSEAEKARRINDEIERQLRRDKRDARRELKLLLTGTGSGKSTFIKQMRIHSGYS 62
QY 65 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIOYMCQENAKIIREVEVDKVTALSRDQ 124
DB 63 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIPKYEHNAHAQLVREVDKVSAPENPY 122
QY 125 VAAIKQLWLDPGTQECYDRRREYQLSDSAKYXLTDIRIAMPSEVPTQDDVLVRVPTTG 184
DB 123 VDAIKSLWDPGTQECYDRRREYQLSDSTKYVNLNLDLRVADPAYLPTQDDVLVRVPTTG 182
QY 185 ITIEYPPDLNPIFRMVDVGGQSRERKWIHCFESVTSIFLVALSEYDQVLAECDNENRM 244
DB 183 ITIEYPPDLQSVIFRMVDVGGQSRERKWIHCFENVTISIMFLVALSEYDQVLVESDNENRM 242
QY 245 EESKALFRITIIYPWFNSVILFNKKDLLEKIMYSHLSVFFPYTPGKQDVKAARDP 304
DB 243 EESKALFRITIIYPWFNSVILFNKKDLLEKIMYSHLSVFFPYTPGQPDQAAREF 302
QY 305 ILKLYDQNDPKRKVIYSHFTCATDTENIRFVFAAVKDTILQNLREFNLV 355
DB 303 ILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQNLKEYNLV 353
RESULT 9
GB11_HUMAN STANDARD; PRT; 359 AA.
AC P29992; Q14350; O15109;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein G(i), alpha subunit (Alpha-11).
GN GN11 OR G11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN SEQUENCE FROM N.A.
RP TISSUE=Retina;
RX MEDLINE=91219481; PubMed=1902575;
RA Jiang M., Pandey S., Tran V.T., Fong H.K.W.;
RT "Guanine nucleotide-binding regulatory proteins in retinal pigment
epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3907-3911(1991).
[2]
RN SEQUENCE FROM N.A.
RP Bai X.H., Acharya R., Bai Y.H., Murtagh J.J.;
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
```

```

[3]
RN SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE OF 244-337 FROM N.A.
RP TISSUE=Hematopoietic;
RX MEDLINP=96077138; PubMed=7492305;
RA Thomas C.P., Dunn M.J., Mattera R.;
RT "Ca2+ signalling in K562 human erythroleukaemia cells: effect of
dimethyl sulphoxide and role of G-proteins in thrombin- and
thromboxane A2-activated pathways.";
RL Biochem. J. 312:151-158(1995).
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; M69013; AAA58624.1; -.
DR EMBL; AF011497; AAB64303.1; -.
DR EMBL; AC005262; AAC25615.1; -.
DR EMBL; L40630; AAA99949.1; -.
DR HIR; A39394; RGHUGY.
DR PSS; P10824; 1BOF.
DR Genew; HGNC:4379; GNA11.
DR MIM; 139313; -.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
KW GTP-binding; Transducer; Multigene family; ADP-ribosylation.
FT NP_BIND 46 53 GTP (BY SIMILARITY).
FT NP_BIND 205 209 GTP (BY SIMILARITY).
FT NP_BIND 274 277 GTP (BY SIMILARITY).
FT MOD_RES 183 183 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT MOD_RES 183 183 (BY SIMILARITY).
FT CONFLICT 6 6 M -> I (IN REF. 2).
FT CONFLICT 266 266 N -> H (IN REF. 4).
FT CONFLICT 285 285 Y -> H (IN REF. 4).
FT CONFLICT 301 302 DA -> EP (IN REF. 1).
FT CONFLICT 310 310 L -> P (IN REF. 2).
SQ SEQUENCE 359 AA; 42123 MW; DD37176589E66046 CRC64;
Query Match 83.4%; Score 1524; DB 1; Length 359;
Best Local Similarity 82.1%; Pred. No. 3.9e-107;
Matches 288; Conservative 35; Mismatches 28; Indels 0; Gaps 0;
QY 5 CCLSAEKEKESQISAEIERHVRDCKDARRELKLLLTGTGSGKSTFIKQMRIHSGYS 64
DB 9 CCLSDVEKESKRINAEIKQLRRDKRDARRELKLLLTGTGSGKSTFIKQMRIHSGYS 68
QY 65 DEDKRGFTKLIVQNIETAMQAMIRAMDTLRIOYMCQENAKIIREVEVDKVTALSRDQ 124
DB 69 EEDKRGFTKLIVQNIETAMQAMIRAMETLKILYKQENKALLIREVDKVTTEHQY 128
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Qy 125 VAAIKQLMDPGIOECYDRRREYQOLSDSAKYLLTDIERIAMPSEVPTQODVLRVRVPTTG 184
Db 129 VSAIKTLMEDPGIOECYDRRREYQOLSDSAKYLLTDVDIRIATLGYLPTQODVLRVRVPTTG 188
Qy 185 IIEYPFDLNIIFRMVDVGGQSRERRKWHCFESVTSIIFLVALSEYDOVLAECDENRM 244
Db 189 IIEYPFDLNIIFRMVDVGGQSRERRKWHCFENVTSMFLVALSEYDOVLVESDENRM 248
Qy 245 EESKALFRTIITYPWFQNSVILFNLKKDLLEEKIMVSHLISYFPYTGPKODVKAARDF 304
Db 249 EESKALFRTIITYPWFQNSVILFNLKKDLLEKILVSHLVYDFPFDPGPDQAAREF 308
Qy 305 ILKLYQDQNPKEKYVSHFTCATDTENIRVFVAAVKDTIQLNLREFNLV 355
Db 309 ILKMFVLDLPDSKIIYSHFTCATDTENIRVFVAAVKDTIQLNLKEYNLV 359

RESULT 10
GBQ_HUMAN
ID GBQ_HUMAN STANDARD; PRT; 353 AA.
AC P50148; Q13462; Q92471; Q15108;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanine nucleotide-binding protein G(q), alpha subunit.
GN GNAQ OR GAQ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96423032; PubMed=8825633;
RA Dong O., Shenker A., Way J., Haddad B.R., Lin K., Hughes M.R.,
RA McBride W.O., Spiegel A.M., Battley J.;
RT "Molecular cloning of human G alpha q cDNA and chromosomal
RT localization of the G alpha q gene (GNAQ) and a processed
RT pseudogene.";
RL Genomics 30:470-475(1995).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96256639; PubMed=8664309;
RA Chen B., Leverette R.D., Schwin D.A., Kwatra M.M.;
RT "Human G(alph a q): cDNA and tissue distribution.";
RL Biochim. Biophys. Acta 1281:125-128(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96433124; PubMed=8836152;
RA Johnson G.J., Leis L.A., Dunlop P.C.;
RT "Specificity of G alpha q and G alpha 11 gene expression in platelets
RT and erythrocytes. Expressions of cellular differentiation and species
RT differences.";
RL Biochem. J. 318:1023-1031(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX Bai X.H., Acharya R., Rivera C., Murtagh J.J.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 74-229 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=93081611; PubMed=1333286;
RA Lesch K.-P., Manji H.K.;
RT "Signal-transducing G proteins and antidepressant drugs: evidence for
RT modulation of alpha subunit gene expression in rat brain.";
RL Biol. Psychiatry 32:549-579(1992).
RN [6]
RP SEQUENCE OF 238-331 FROM N.A.
RC TISSUE=Hematopoietic;
RX MEDLINE=96077138; PubMed=7492305;
RA Thomas C.P., Dunn M.J., Mattern R.;
RT "Ca2+ signalling in K562 human erythroleukaemia cells: effect of
RT dimethyl sulphoxide and role of G-proteins in thrombin- and
```

```
thromboxane A2-activated pathways.";
Biochem. J. 312:151-158(1995).
-1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS.
-1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
-1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN OVARY, PROSTATE,
TESTIS AND COLON.
-1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
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EMBL; U40038; AAC50363.1; ALT_INIT.
EMBL; U43083; AAB06875.1; ALT_INIT.
EMBL; L76256; AAB39498.1; ALT_INIT.
EMBL; AF011496; AAB64301.1; ALT_INIT.
EMBL; L40629; AAG99950.1; -.
HSSP; P10824; IBOF.
GeneW; HGNC:4390; GNAQ.
MIN; 600998; -.
InterPro: IPR001019; Gproteins_alpha.
Pfam; PF00503; G-alpha; 1.
PRINTS; PR00318; GPROTEIN.
PRODOM; PD000281; Gproteins_alpha; 1.
SMART; SM00275; G-alpha; 1.
GTP-binding; Transducer; Multigene family; ADP-ribosylation;
Palmitate; Lipoprotein.
LIPID 3
LIPID 4 4
NP_BIND 40 47
NP_BIND 199 203
NP_BIND 268 271
MOD_RES 177 177
CONFLICT 22 23
CONFLICT 86 86
CONFLICT 97 97
CONFLICT 165 165
CONFLICT 318 318
CONFLICT 331 331
CONFLICT 352 352
SEQUENCE 353 AA; 41425 MW; E7798E07B1F4904C CRC64;
Query Match 83.1%; Score 1519; DB 1; Length 353;
Best Local Similarity 81.2%; Pred. No. 9.1e-107;
Matches 285; Conservative 36; Mismatches 30; Indels 0; Gaps 0;
Qy 5 CCLSAEKEESORISAEIERHVRDRKDKARRELKLLLLGTGESGKSTFFIKQMRIHSGYS 64
Db 3 CCLSEAEKARRINDEIERLRDRKDRARRELKLLLLGTGESGKSTFFIKQMRIHSGYS 62
Qy 65 DEDRKGFTKLYQNIFTAMQAMIRAMDTLRTOYMCQENKQNAQIIRREVQKVTALSRDQ 124
Db 63 DEDKRGFTKLYQNIFTAMQAMIRAMDTLRTPYKYEHNKAQALQVREVDKVSAPENPY 122
Qy 125 VAAIKQLMDPGIOECYDRRREYQOLSDSAKYLLTDIERIAMPSEVPTQODVLRVRVPTTG 184
Db 123 VDAIKSLWDPGIOECYDRRREYQOLSDSTKYLLDRLDRAVDPAVLPPTQODVLRVRVPTTG 182
Qy 185 IIEYPFDLNIIFRMVDVGGQSRERRKWHCFESVTSIIFLVALSEYDOVLAECDENRM 244
Db 183 IIEYPFDLQSVIFRMVDVGGQSRERRKWHCFENVTSMFLVALSEYDOVLVESDENRM 242
Qy 245 EESKALFRTIITYPWFQNSVILFNLKKDLLEEKIMVSHLISYFPYTGPKODVKAARDF 304
Db 243 EESKALFRTIITYPWFQNSVILFNLKKDLLEEKIMVSHLVYDFPFDPGPDQAAREF 302
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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RN RP
 RA LADNER K.J., Smith L.D.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=94298961; PubMed=8026589;
 RA Shapiro H., Way J., Lipinsky D., Oron Y., Battay J.F.;
 RT "Neuremodin B receptor, expressed in Xenopus laevis oocytes,
 RT selectively couples to G alpha q and not G alpha 11.";
 FEBS Lett. 348:89-92(1994).
 RN [3]
 RN RP ERRATUM.
 RA Shapiro H., Way J., Lipinsky D., Oron Y., Battay J.F.;
 RL FEBS Lett. 349:318-318(1994).
 CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.
 CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA). THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
 CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).

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EMBL; L05540; AAA49730.1; ALT_INIT.
 EMBL; U10502; AAA52189.1; ALT_INIT.
 HSSP; P10824; 1BOF.

InterPro: IPR001019; Gprotein_alpha.
 Pfam: PF00503; G-alpha; 1.
 PRINTS; PR00318; GPROTEIN.
 ProDom; PD000281; Gprotein_alpha; 1.
 SMART; SM00275; G-alpha; 1.
 KW GTP-binding; Transducer; Multigene family; ADP-ribosylation;
 KW Palmitate; Lipoprotein.

FT	LIPID	3	3	PALMITATE (BY SIMILARITY).
FT	LIPID	4	4	PALMITATE (BY SIMILARITY).
FT	NP_BIND	40	47	GTP (BY SIMILARITY).
FT	NP_BIND	199	203	GTP (BY SIMILARITY).
FT	NP_BIND	268	271	GTP (BY SIMILARITY).
FT	MOD_RES	177	177	ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT				(BY SIMILARITY).
FT	CONFLICT	10	10	E -> K (IN REF. 2).
FT	CONFLICT	79	79	S -> T (IN REF. 2).
FT	CONFLICT	158	158	L -> V (IN REF. 2).
FT	CONFLICT	164	164	H -> Q (IN REF. 2).
FO	SEQUENCE	353 AA;	41541 MW;	2310142412184553 CRC64;

Query Match 81.6%; Score 1492; DB 1; Length 353;
 Best Local Similarity 80.1%; Pred. No. 9.5e-105;
 Matches 281; Conservative 37; Mismatches 33; Indels 0; Gaps 0;

QY 5 CCLSAEKEQSRIQSAETIERHVRKDKDARELKILLGLGTGESKGSTFIKMRIHSGYS 64
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 3 CCLSEAEARRINDEIERQLRDQRARELKILLGLGTGESKGSTFIKMRIHSGYS 62

QY 65 DEBKRGFTKLVYQNIFAMQAMIRAMDTLRIQVMCEQNKENAQIIREVDKVTASRDQ 124
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 63 DEBKRGFTKLVYNIFSAMQAMIRAMETLTPIPKYEHNKHALLVREVDVKASFENPY 122

QY 125 VAAIKQLWDPGTOECYDRRERVLSDSAKYLLTDIERIAMPEVFPTQQDLRVRPVTTG 184
 ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
 Db 123 VDAIKYLWNDPGTOECYDRRERVLSDSKTYLLNLDRIATHGYLPQTQQDLRVRPVTTG 182

QY 185 IIEYFDLENIIFRMVDVGQSRERKWIHCFSVTSIIIFLVALSEYDQVLAECNENRM 244
Db 183 IIEYFDLQSVIFRMVDVGQSRERKWIHCENVTSIMFLVALSEYDQVLVESDNENRM 242
QY 245 EESKALFRTIITYPWFNLSSVILFLNKKDILLEEKIMYSHLISYFPEYTGPKQDVKAARDP 304
Db 243 EESKALFRTIITYPWFQNSSVILFLNKKDILLEEKIMYSHLVDFPEYDGPORDAQAAREF 302
QY 305 ILKLYODQNPDKVKIYSHFTCATDTENIRFVFAAVKDTILOLNREFNLV 355
Db 303 ILKMFVDLNPDSDKIYSHFTCATDTENIRFVFAAVKDTILOLNKEYNLV 353

Search completed: February 3, 2003, 14:11:42
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 3, 2003, 14:04:16 ; Search time 35 Seconds
(without alignments)
2089.906 Million cell updates/sec

Title: US-09-492-028-2
Perfect score: 1828
Sequence: 1 MAGCCCLSAEKEQSRIASAE.....VFAAVKDTIQLNLREFNLV 355

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1817	99.4	355	11	Q8R2X9 mus musculus
2	1524	83.4	359	4	Q9BZB9 homo sapien
3	1498	81.9	359	11	Q91X95 mus musculus
4	1435	78.5	353	5	P91955 limulus pol
5	1410	77.1	353	5	Q9U473 panulirus a
6	1408	77.0	355	5	Q17386 caenorhabdi
7	1388	75.9	353	5	Q9AL92 octopus vul
8	1385	75.8	353	5	Q8T6P8 mamestra br
9	1356	74.2	353	5	Q9NF20 calliphora
10	1352	74.0	360	5	Q8WSU8 halocynthia
11	1215	66.5	303	5	Q8T3G5 caenorhabdi
12	1123.5	61.5	305	5	Q9V207 hydra magni
13	1065.5	58.3	355	5	Q9XZV4 geodia cydo
14	1028	56.2	279	5	Q917C8 drosophila
15	1011	55.3	374	6	Q9TU29 oryctolagus
16	907.5	49.6	354	4	Q8TD72 homo sapien

17	892.5	48.8	354	13	Q90847
18	891.5	48.8	354	4	Q9UGA4
19	888.5	48.6	354	13	O13011
20	884.5	48.4	354	13	Q90846
21	883	48.3	355	13	Q9W6A4
22	882	48.2	355	4	Q96C71
23	879.5	48.1	354	4	O8TAN5
24	878.5	48.1	354	11	O9DC51
25	876	47.9	350	13	O93565
26	875	47.9	305	5	O9Y203
27	872	47.7	353	3	Q96VA7
28	872	47.7	353	3	Q96T18
29	872	47.7	353	3	O8TGA3
30	869	47.5	353	3	O96VN7
31	868.5	47.5	354	5	O9NL93
32	867.5	47.5	301	5	O9Y202
33	866	47.4	353	3	O9HFA2
34	866	47.4	353	3	Q9C134
35	864.5	47.3	354	13	O93564
36	863	47.2	371	13	O8QGY8
37	861	47.1	357	5	O9NL97
38	855	46.8	469	5	O8WPA0
39	852	46.6	353	3	O9HEP9
40	850.5	46.5	354	5	O8WP45
41	848.5	46.4	354	3	O9HFN1
42	842.5	46.1	350	13	O9DG28
43	840.5	46.0	354	5	O9NL94
44	840.5	46.0	354	5	O8WSS1
45	838	45.8	354	3	O9C115

ALIGNMENTS

RESULT 1

ID	Q8R2X9	PRELIMINARY;	PRT;	355 AA.
AC	Q8R2X9;			
DT	01-JUN-2002 (TremBLrel. 21, Created)			
DT	01-JUN-2002 (TremBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TremBLrel. 21, Last annotation update)			
DE	Guanine nucleotide binding protein, alpha 14.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC027015; AAH27015.1; -			
SQ	SEQUENCE 355 AA; 41527 MW; D34B39ACD179AE82 CRC64;			

Query Match 99.4%; Score 1817; DB 11; Length 355;
Best Local Similarity 99.4%; Pred. No. 46-136;
Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MAGCCCLSAEKEQSRIASAEIERHVRDKDARRELKLLLLCTGSGSKSTFIKOMRIHG	60
Db	1	MAGCCCLSAEKEQSRIASAEIERHVRDKDARRELKLLLLCTGSGSKSTFIKOMRIHG	60
Qy	61	SGYSDEDRGFTKLVYQNTFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTAL	120
Db	61	SGYSDEDRGFTKLVYQNTFTAMQAMIRAMDTLRIOYMCQENKNAQIIREVEVDKVTAL	120
Qy	121	SRDQVAAIKOLMWDPCIQCYRRREYQLSDSAKYLYLTDIERTAMPSPFVPTQDDVLVRV	180
Db	121	SRDQVAAIKOLMWDPCIQCYRRREYQLSDSAKYLYLTDIERTAMPSPFVPTQDDVLVRV	180
Qy	181	PTGTIIIEYFPDLENIIFRMVDVGGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECN	240
Db	181	PTGTIIIEYFPDLENIIFRMVDVGGQSRERRKWIHCFSVTSIIFLVALSEYDQVLAECN	240

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QY 241 ENRWEESKALFRTIITYPWFLNSVILFLNKKDLLLEKIMYSHLISYFFPYTGPKQDVKA 300
Db 241 ENRWEESKALFRTIITYPWFLNSVILFLNKKDLLLEKIMYSHLISYFFPYTGPKQDVKA 300
QY 301 ARDFILKLYQDQNPDKVKYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 301 ARDFILKLYQDQNPDKVKYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355

RESULT 2
Q9BZB9 PRELIMINARY; PRT; 359 AA.
ID Q9BZB9
AC Q9BZB9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE G alpha q protein (Guanine nucleotide binding protein alpha q).
GN GNAQ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9605;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98366208; PubMed=9700850;
RA Gabbeta J., Dhanasekaran N., Rao A.K.;
RT "G alpha q cDNA sequence from human platelets.";
RL Thromb. Res. 91:29-32(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Gabbeta J., Dhanasekaran N., Rao A.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "Homo sapiens guanine nucleotide binding protein (G protein) alpha q
(cNAQ).";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF329284; AAG61117.1; -.
DR EMBL; AF493896; AAM12610.1; -.
DR HSSP; P10824; IBOF.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
SQ SEQUENCE 359 AA; 42142 MW; 6F69C4F617DFA7C7 CRC64;

Query Match 83.4%; Score 1524; DB 4; Length 359;
Best Local Similarity 81.5%; Pred. No. 7e-113;
Matches 286; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 5 CCLSAEESQRTSAETIERHVRDKKARRELKLLLGTSKSTFIKQRIIHGSGYS 64
Db 9 CCLSEAEKARRINDELERQKRDARRELKLLLGTSKSTFIKQRIIHGSGYS 68
QY 65 DEDKRGFTKLIVQNIPTAQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTALSRDQ 124
Db 69 DEDKRGFTKLIVQNIPTAQAMIRAMDTLKIPIYEHKHAQVLVREVDVKEVSAPENY 128
QY 125 VAAIKQLWLDPGTQECYDRREYQSDSAKYILTDTERIAMPFVPTQDVLVRVPTTG 184
Db 129 VDAIKLWLDPGTQECYDRREYQSDSTKYILNDLRVADPAFLPTQDVLVRVPTTG 188
QY 185 IIEYFPDLENIIFRMVDVGQSRERRKWIHCFESVTSIIFLVALSEYDQVLAECDNENRM 244
Db 189 IIEYFPDLSQVIFRMVDVGQSRERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRM 248
QY 245 EESKALFRTIITYPWFLNSVILFLNKKDLLEKIMYSHLISYFFPYTGPKQDVKAARD 304
Db 249 EESKALFRTIITYPWFQNSVILFLNKKDLLEKIMYSHLVDFYFPEFDGPDQQAAREF 308
QY 305 ILKLYQDQNPDKVKYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355

Query Match 81.9%; Score 1498; DB 11; Length 359;
Best Local Similarity 80.3%; Pred. No. 8.1e-111;
Matches 282; Conservative 38; Mismatches 31; Indels 0; Gaps 0;

QY 5 CCLSAEESQRTSAETIERHVRDKKARRELKLLLGTSKSTFIKQRIIHGSGYS 64
Db 9 CCLSDVEKESKRINAELEKOLRRDKRDARRELKLLLGTSKSTFIKQRIIHGAGYS 68
QY 65 DEDKRGFTKLIVQNIPTAQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTALSRDQ 124
Db 69 EEDKRGFTKLIVQNIPTAQAMVIRAMATLKILYKQNKANALLIREVDLEKVTTFHQY 128
QY 125 VAAIKQLWLDPGTQECYDRREYQSDSAKYILTDTERIAMPFVPTQDVLVRVPTTG 184
Db 129 VNAIKTLWSDPGVQECYDRRPEFQSDSAKYILTDVRIATVGLPTQQDVLVRVPTTG 188
QY 185 IIEYFPDLENIIFRMVDVGQSRERRKWIHCFESVTSIIFLVALSEYDQVLAECDNENRM 244
Db 189 IIEYFPDLENIIFRMVDVGQSRERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRM 248
QY 245 EESKALFRTIITYPWFLNSVILFLNKKDLLEKIMYSHLISYFFPYTGPKQDVKAARD 304
Db 249 EESKALFRTIITYPWFQNSVILFLNKKDLLEKIMYSHLVDFYFPEFDGPDQQAAREF 308
QY 305 ILKLYQDQNPDKVKYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 309 ILKMFVDLPDSDKIYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 359

RESULT 4
P91955 PRELIMINARY; PRT; 353 AA.
ID P91955
AC P91955
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Gq protein alpha subunit.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENTRAL EYE;
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Db 309 ILKMFVDLPDSDKIYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 359

RESULT 3
Q91X95 PRELIMINARY; PRT; 359 AA.
ID Q91X95
AC Q91X95
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to guanine nucleotide binding protein, alpha 11.
GN GNAL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011169; AAH11169.1; -.
DR MGD; MGI:95766; Gnal1.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
DR ProDom; PD000281; Gprotein_alpha; 1.
SQ SEQUENCE 359 AA; 41930 MW; 7437912FF0BAC855 CRC64;

Query Match 81.9%; Score 1498; DB 11; Length 359;
Best Local Similarity 80.3%; Pred. No. 8.1e-111;
Matches 282; Conservative 38; Mismatches 31; Indels 0; Gaps 0;

QY 5 CCLSAEESQRTSAETIERHVRDKKARRELKLLLGTSKSTFIKQRIIHGSGYS 64
Db 9 CCLSDVEKESKRINAELEKOLRRDKRDARRELKLLLGTSKSTFIKQRIIHGAGYS 68
QY 65 DEDKRGFTKLIVQNIPTAQAMIRAMDTLRIQYMCQNKENAOIIRVEVDKVTALSRDQ 124
Db 69 EEDKRGFTKLIVQNIPTAQAMVIRAMATLKILYKQNKANALLIREVDLEKVTTFHQY 128
QY 125 VAAIKQLWLDPGTQECYDRREYQSDSAKYILTDTERIAMPFVPTQDVLVRVPTTG 184
Db 129 VNAIKTLWSDPGVQECYDRRPEFQSDSAKYILTDVRIATVGLPTQQDVLVRVPTTG 188
QY 185 IIEYFPDLENIIFRMVDVGQSRERRKWIHCFESVTSIIFLVALSEYDQVLAECDNENRM 244
Db 189 IIEYFPDLENIIFRMVDVGQSRERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRM 248
QY 245 EESKALFRTIITYPWFLNSVILFLNKKDLLEKIMYSHLISYFFPYTGPKQDVKAARD 304
Db 249 EESKALFRTIITYPWFQNSVILFLNKKDLLEKIMYSHLVDFYFPEFDGPDQQAAREF 308
QY 305 ILKLYQDQNPDKVKYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
Db 309 ILKMFVDLPDSDKIYIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 359

RESULT 4
P91955 PRELIMINARY; PRT; 353 AA.
ID P91955
AC P91955
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Gq protein alpha subunit.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENTRAL EYE;
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RA Munger S.D., Schremser-Berlin J.-L., Brink C.M., Battelle B.-A.;
RT "Molecular and Immunological Characterization of a Gq Protein from
RL Ventral and Lateral Eye of the Horseshoe Crab Limulus polyphemus.";
DR Invert. Neurosci. 0:0-0(1997).
DR EMBL: U88586; AAB48510.1; -.
DR HSSP: P10824; 1BOF.
DR InterPro: IP0001019; Gprotein_alpha.
DR Pfam: PF00503; G-alpha; 1.
DR PRINTS: PR00318; GPROTEINA.
DR ProDom: PD000281; Gprotein_alpha; 1.
DR SMART: SM00275; G-alpha; 1.
SQ SEQUENCE 353 AA; 41497 MW; CLC57783B3D2D516 CRC64;

Query Match 78.5%; Score 1435; DB 5; Length 353;
Best Local Similarity 76.6%; Pred. No. 7.8e-106;
Matches 269; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

QY 5 CCLSAEESQRTSABIERHVRDKDARRELKLLGLTGSGSKSTFIKMRHIGSGYS 64
DB 3 CCLSECKEQKRINQERQLRKDRARRELKLLGLTGSGSKSTFIKMRHIGSGYS 62

QY 65 DEDKRGFTKLIVYONITAMQAMIRAMDTLRIOVMCEQNKENAOIIEVEVDKVTALSRDQ 124
DB 63 DDDKRSIKLVYONITAMQSMKAMKMLKISYKDRNNIENAEVLVSVDYETVTTDPSY 122

QY 125 VAAIKQLWDPGQIECYDRRREYQLSDSAKYLYLTDIERIAMPSEVPTQDVLRRVPTTG 184
DB 123 VEAIKSLWDPGQIECYDRRREYQLSDSAKYLYLTDIATVNPYLTQDILRRVPTTG 182

QY 185 IIEYFPLENIIFRMVDVGQSRERKWIHCFESVTSIIIFLVALSEYDQVLAECNENRM 244
DB 183 IIEYFPLENIIFRMVDVGQSRERKWIHCFENVTIIIFLVALSEYDQVLAECNENRM 242

QY 245 EESKALFRITIIYPWFLNSVILFLNKKDLLEKIMYSHLISYFPEYTGPKQDVKAARDP 304
DB 243 EESKALFKITIIYPWFLNSVILFLNKKDLLEKIMYSHLVDYFPEYTGPKDAVQGRE 302

QY 305 ILKLYODQNPDEKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
DB 303 ILKMFVLDLPDSEKIIYSHFTCATDTENIRFVFAAVKDTILQNLNKEYNLV 353

RESULT 5
Q9U473 PRELIMINARY; PRT; 353 AA.
AC Q9U473;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Gq/11 protein alpha subunit.
OS Panulirus argus (Spiny lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuroidea; Palinuridae; Panuliridae; Panulirus.
OX NCBI_TaxID=6737;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OLFACTORY ORGAN;
RX MEDLINE=20347127; PubMed=10781594;
RA Munger S.D., Gleeson R.A., Aldrich H.C., Rust N.C., Ache B.W.,
RA Greenberg R.M.;
RT "Characterization of a phosphoinositide-mediated Odor transduction
RT pathway reveals plasma membrane localization of an inositol 1,4,5-
RT triphosphate receptor in lobster olfactory receptor neurons.";
RL J. Biol. Chem. 275:20450-20457(2000).
DR EMBL: AF201328; AAF19378.1; -.
DR HSSP: P10824; 1BOF.
DR InterPro: IP0001019; Gprotein_alpha.
DR Pfam: PF00503; G-alpha; 1.
DR PRINTS: PR00318; GPROTEINA.
DR ProDom: PD000281; Gprotein_alpha; 1.
DR SMART: SM00275; G-alpha; 1.
SQ SEQUENCE 353 AA; 41478 MW; FD9B551F66327BAA CRC64;

Query Match 77.1%; Score 1410; DB 5; Length 353;
Best Local Similarity 76.1%; Pred. No. 7.5e-104;
Matches 267; Conservative 37; Mismatches 47; Indels 0; Gaps 0;

QY 5 CCLSAEESQRTSABIERHVRDKDARRELKLLGLTGSGSKSTFIKMRHIGSGYS 64
DB 3 CCLSECKEQKRINQERQLRKDRARRELKLLGLTGSGSKSTFIKMRHIGSGYS 62

QY 65 DEDKRGFTKLIVYONITAMQAMIRAMDTLRIOVMCEQNKENAOIIEVEVDKVTALSRDQ 124
DB 63 DEDKRGFTKLIVYONITAMQSMKAMKMLKISYKDRNNIENAEVLVSVDYETVTTPEPY 122

QY 125 VAAIKQLWDPGQIECYDRRREYQLSDSAKYLYLTDIERIAMPSEVPTQDVLRRVPTTG 184
DB 123 VTAIKSLWDPGQIECYDRRREYQLSDSAKYLYLTDIATVNPYLTQDILRRVPTTG 182

QY 185 IIEYFPLENIIFRMVDVGQSRERKWIHCFESVTSIIIFLVALSEYDQVLAECNENRM 244
DB 183 IIEYFPLENIIFRMVDVGQSRERKWIHCFENVTIIIFLVALSEYDQVLAECNENRM 242

QY 245 EESKALFRITIIYPWFLNSVILFLNKKDLLEKIMYSHLISYFPEYTGPKQDVKAARDP 304
DB 243 EESKALFKITIIYPWFLNSVILFLNKKDLLEKIMYSHLVDYFPEYTGPKDAIAAREF 302

QY 305 ILKLYODQNPDEKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNLV 355
DB 303 ILKMFVLDLPDSEKIIYSHFTCATDTENIRFVFAAVKDTILQNLNKEYNLV 353

RESULT 6
Q17386 PRELIMINARY; PRT; 355 AA.
AC Q17386; O02546;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE EGL-30 (HETEROTRIMERIC G protein alpha subunit).
GN EGL-30 OR M01D7.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=96221161; PubMed=8630258;
RA Brundage L., Avery L., Katz A., Kim U.J., Mendel J.E., Sternberg P.W.,
RA Simon M.I.;
RT "Mutations in a C. elegans Gqalpha gene disrupt movement, egg laying,
RT and viability".
RL Neuron 16:999-1009(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smalton N., Smith A., Sonnhammer E., Staden K., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watsoy A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans".
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Gattung S., Goela D., Wilson R.;

Qy	125	VAAIKQLWLDPG	IOECYDRRREYQLSDSAKYYLTDIERTAMPSEVPTQODVLVRVPTTG	181				
Db	123	VEAIKALWADAG	IOECYDRRREYQLTDSAKYYLQEIADRAAPNLYLPTQDILVRVLTG	182				
Qy	185	IIIEYPPDLENI	IFRMVDVGQSRERRKWIHCFESVTSIIIFLVALSEYDQVLAECNDENRM	244				
Db	183	IIIEYPPDLENI	IFRMVDVGQSRERRKWIHCFENVTIIIFLVALSEYDQILFESDENRM	242				
Qy	245	EESKALFRTIITY	PWFNLSSVILFLNKKDLLEEKIMYSHLISYFPETGPKQDVKAAARDF	304				
Db	243	EESKALFRTIITY	PWFQHSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQDANTAREF	302				
Qy	305	ILKLYQDQNDP	KEKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNL	354				
Db	303	ILRTFVLDNPD	AEKIIYSHFTCATDTENIKLVCAVKDTIMQALKEFNL	352				
RESULT 9								
ID	Q9NF20	PRELIMINARY;	PRT;	353 AA.				
AC	Q9NF20;							
DT	01-OCT-2000	(T=EMBLrel. 15, Created)						
DT	01-OCT-2000	(T=EMBLrel. 15, Last sequence update)						
DT	01-MAR-2002	(T=EMBLrel. 20, Last annotation update)						
DE	Guanine nucleotide-binding protein alpha subunit.							
OS	Calliphora vicina (Blue blowfly) [Calliphora erythrocephala].							
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;							
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;							
OC	Oestroidea; Calliphoridae; Calliphora.							
OX	NCBI_TaxID=7373;							
RN	[1]							
RC	SEQUENCE FROM N.A.							
RA	TISSUE=EYE;							
RA	Schulz S., Huber A., Schwab K., Paulsen R.;							
RT	"A novel Ggamma isolated from Drosophila constitutes a visual G							
RT	protein gamma subunit of the fly compound eye.";							
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.							
DR	EMBL;	AJ250443;	CAB76453.1;	-				
DR	HSSP;	P10824;	1BOF.					
DR	InterPro;	IPR001019;	Gprotein_alpha.					
DR	Pfam;	PF00503;	G-alpha:1.					
DR	PRINTS;	PR00318;	GPROTEINA.					
DR	ProDom;	PD000281;	Gprotein_alpha:1.					
DR	SMART;	SM00275;	G-alpha:1.					
SQ	SEQUENCE 353 AA; 41295 MW; FFF799774C02072E CRC64;							
Query Match 74.2%; Score 1356; DB 5; Length 353;								
Best Local Similarity 72.9%; Pred. No. 1.4e-99;								
Matches 255; Conservative 41; Mismatches 54; Indels 0; Gaps								
Qy	5	CCLSAEAKESQRI	SAEIERHVRKDKDARRELKLLLGTTGESGKSTFIKQRIIHSGYS	64				
Db	3	CCLSEAEKQKRI	NOEIERQLRRDKDARRELKLLLGTTGESGKSTFIKQRIIHSGYS	62				
Qy	65	DEDRKGTFLVYQNI	FAMQAMTRAMDTLRIQWCEQNKENAKIIRREVVDKVTALSRDQ	124				
Db	63	DDDRRGYIKLVQ	IFNIFAMQSMIKAMDMLRISYGARDHAELALVMSIDYETVTSFDPY	122				
Qy	125	VAAIKQLWLDPG	IOECYDRRREYQLSDSAKYYLTDIERTAMPSEVPTQODVLVRVPTTG	184				
Db	123	LSAIKTLWADG	IOECYDRRREYQLTDSAKYYLSLIEREQADILFSEQDILARVPTTG	182				
Qy	185	IIIEYPPDLENI	IFRMVDVGQSRERRKWIHCFESVTSIIIFLVALSEYDQVLAECNDENRM	244				
Db	183	IIIEYPPDLENI	IFRMVDVGQSRERRKWIHCFENVTIIIFLVALSEYDQILFESDENRM	242				
Qy	245	EESKALFRTIITY	PWFNLSSVILFLNKKDLLEEKIMYSHLISYFPETGPKQDVKAAARDF	304				
Db	243	EESKALFRTIITY	PWFQHSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQDHAARKQF	302				
Qy	305	ILKLYQDQNDP	KEKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREFNL	354				
Db	303	VLKYYLAAPPD	PEQCYSHFTAFDTENIKLVCAVKDTIMQALKEFNL	352				

RESULT 10

Q8WSU8		PRELIMINARY;	PRT;	360 AA.
ID	Q8WSU8			
AC	Q8WSU8;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	G protein alpha subunit q class.			
GN	HKGQ.			
OS	Halocynthia roretzi (Sea squirt).			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;			
OC	Stolidobranchia; Pyuridae; Halocynthia.			
RN	NCBI_TaxID=7729;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RT	Iwasa T., Kanehara K., Watari A., Ohkuma M., Tsuda M.;			
RT	"Cloning and expression patterns of G proteins in the larvae of			
RL	Halocynthia roretzi."			
RL	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AB047084; BAB79199.1; -			
DR	InterPro: IPR001019; Gprotein_alpha.			
DR	Pfam; PF00503; G-alpha_1.			
DR	PRINTS; PR00316; GPROTEINA.			
DR	ProDom; PD000281; Gprotein_alpha; 1.			
DR	SMART; SM00275; G-alpha; 1.			
SQ	SEQUENCE 360 AA; 42571 MW; A4ECFB6AE3C56DC9 CRC64;			

Query Match 74.0%; Score 1352; DB 5; Length 360;
Best Local Similarity 73.1%; Pred. No. 3.1e-99;
Matches 258; Conservative 40; Mismatches 53; Indels 2; Gaps

Qy	5	CCLSAEEKSORISAEIERHVRDDKKDARRELLKLLGTGSGSKSTFIKOMRIHGSGYS	64
Dd	8	CKSEQEAKRNAIEERELRRHKRDARRELLKLLGTGSGSKSTFIKOMRIHGKGS	67
Qy	65	DEDKRGFTKLIVQNIFAMQAMIRAMDTRLIQIYCEONKENAQIIREVEVDKYTALS--R	122
Dd	68	DNDRREFCKLVHQNLITSMQNNIRAMETLHIQYSDPQNEQNSDFLELDVRAEQNGFP	127
Qy	123	DOVAAIKQLWDPGIQCYYDRRREYQLSDSAKYLTDIERIA MPSFVPTQQDVLRVRVP	182
Dd	128	EYCTAIEALWDKGIHCYDRREYQLSDSTSYLYNSLDIRMPDYLPTEQDVLRVRVP	187
Qy	183	TGITIYPFDLENIIFRMVDVGQSRERKWHCFESVTSIFIIVALSEYDQVLAECDNEN	242
Dd	188	TGISIYEPFDLSIIIFRMVDVGQSRERKWHCFENVTSIMFLVALSEYDQVLVESNEN	247
Qy	243	RMEESKALFFITIYPFNLSNVTLFNKKDLLEEKIMYSHLISYPEYTGPKQDVKAAR	302
Dd	248	RMEESKALFFITIYPFNQSSVILFNKKDLLEEKIMYSHLDYFSYDGPQTQANAAR	307
Qy	303	DFILKLYQDQNPKEKIYSHFTCATDTENIRVFVAAVKOTILQLNLREYNLV	355
Dd	308	EFILSRFVELNPDADKIVISHFTCATDTENIRVFVAAVKOTILQCNLREYNLV	360

RESULT 11

Q8T3G5		PRELIMINARY;	PRT;	303 AA.
ID	Q8T3G5			
AC	Q8T3G5;			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DE	C. elegans EGL-30 protein (corresponding sequence M01D7.7b).			
GN	EGL-30.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
RN	NCBI_TaxID=6235;			
RP	[1]			
RP	SEQUENCE FROM N.A.			

```
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Gattung S., Goela D.;
RT "The sequence of C. elegans cosmid M01D7.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF003739; AAM15593.1; -. 12B5A76956116D28 CRC64;
SQ SEQUENCE 303 AA; 35807 MW; 12B5A76956116D28 CRC64;

Query Match 66.5%; Score 1215; DB 5; Length 303;
Best Local Similarity 74.9%; Pred. No. 1.8e-88;
Matches 227; Conservative 38; Mismatches 36; Indels 2; Gaps 1;

QY 55 MRIIHGYSDEDRKGFVKLVYQNIETAMQAMIRAMDTLRIQY--MCQNKENAOIIEVEV 112
DB 1 MRIIHGQGYSEEDKRAHRLKLVYQNYFMATQSMIRAMDTLDIKFEGNESEELQKAAVREV 60
QY 113 EYDKVTALSRDQVAAIKQLWLDPGICQYDRRREYQLSDSAKYILTDTIERIAMPSPVPTQ 172
DB 61 DFESVTSPEPVSYIKELWEDSGIQCYDRRREYQLSDSAKYILSDRLRLAVPYLPIE 120
QY 173 QDVLVRVPTTGIIIEYPPFDLENIIFRMVDVGGQSRERRKWIHCFESVTSIIFLVALSEYD 232
DB 121 QDILVRVPTTGIIIEYPPFDLENIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYD 180
QY 233 QVLAECNENRMEESKALPRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYEPT 292
DB 181 QVLVECDNENRMEESKALPRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLADYFPEYD 240
QY 293 GPKQDYKAARDFILKLYQDNPKDKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREF 352
DB 241 GPPROPIAREFILKMFVDLPNADKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREF 300
QY 353 NLV 355
DB 301 NLV 303

RESULT 12
QYI207
ID Q9Y207 PRELIMINARY; PRT; 305 AA.
AC Q9Y207;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-WAR-2002 (TReMBLrel. 20, Last annotation update)
DE G protein a subunit 3 (fragment).
OS Hydra magnipapillata (Hydra).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6085;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99246375; PubMed-10229568;
RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA Miyata T.;
RT "Extensive gene duplication in the early evolution of animals before
the parazoan-eumetazoan split demonstrated by G proteins and protein
tyrosine kinases from sponge and hydra.";
RL J. Mol. Evol. 48:646-653(1999).
DR EMBL: AB006541; BAA81695.1; -.
DR HSSP: P10824; 1BOF.
DR InterPro: IPR001019; Gprotein_alpha.

Query Match 58.3%; Score 1065.5; DB 5; Length 355;
Best Local Similarity 59.2%; Pred. No. 1.6e-76;
Matches 206; Conservative 53; Mismatches 88; Indels 1; Gaps 1;

QY 5 CCLSAEEKSQISAEIERHVRDKKARRELKLLLLGTGSGKSTFTTKQMRIIHGSGYS 64
DB 3 CLLSEERLQKRINRINRELQDHKDAKKEIKLLLLGTGSGKSTFTTKQMRIIHGSGYS 62

DR PFam: PF00503; G-alpha; 1.
DR PRINTS: PR00318; GPROTEINA.
DR PRODom: PD000281; Gprotein_alpha; 1.
DR SMART: SM00275; G-alpha; 1.
FT NON_TER 1
SQ SEQUENCE 305 AA; 35491 MW; 26399884D438586E9 CRC64;

Query Match 61.5%; Score 1123.5; DB 5; Length 305;
Best Local Similarity 70.8%; Pred. No. 3.3e-81;
Matches 216; Conservative 38; Mismatches 46; Indels 5; Gaps 2;

QY 56 RIIHSGYSDEDRKGFVKLVYQNIETAMQAMIRAMDTLRIQYMCQNKENAOIIEVEV- 114
DB 1 RIIHGGYGTEDDRRGYTNLVLNIYQAOALTRAMRLKISYSPANEENARLILDVDS 60
QY 115 -DK---VTALSRDQVAAIKQLWLDPGICQYDRRREYQLSDSAKYILTDTIERIAMPSPVFP 170
DB 61 EDKSRITITLSPQYASAIESLWKDSGICQYDRRREYQLSDSAKYILSDRLKICAPNFVP 120
QY 171 TOQDVLVRVPTTGIIIEYPPFDLENIIFRMVDVGGQSRERRKWIHCFESVTSIIFLVALSE 230
DB 121 TMQDVLRARAPTGIIEYPPFDLENIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSE 180
QY 231 YDOVLAECNENRMEESKALPRTIITYPWFNLSSVILFLNKKDLLEEKIMYSHLISYPE 290
DB 181 YDQVLFESQSENRMDESALFKTIITYPWFLOSSILFLNKKDLLEEKIQKSDLOQTYPPE 240
QY 291 YTGPKQDYKAARDFILKLYQDNPKDKVIYSHFTCATDTENIRFVFAAVKDTILQNLNREF 350
DB 241 YDGAAGDAKAAEFILKMFVDLPNADKIIYSHFTCATDTENIRFVFAAVKDTILQNLNREF 300
QY 351 ENLV 355
DB 301 EYNLV 305

RESULT 13
Q9XZV4
ID Q9XZV4 PRELIMINARY; PRT; 355 AA.
AC Q9XZV4;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-WAR-2002 (TReMBLrel. 20, Last annotation update)
DE Gq protein, alpha subunit.
GN GQ.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98119577; PubMed-9459489;
RA Seack J., Kruse M., Mueller W.E.G.;
RT "Evolutionary analysis of G-protein in early metazoans: Cloning of
alpha- and beta-subunits from the sponge Geodia cydonium.";
RL Biochim. Biophys. Acta 1401:93-103(1998).
DR EMBL: Y14248; CAB43527.1; -.
DR HSSP: P04896; IAZT.
DR InterPro: IPR001019; Gprotein_alpha.
DR PFam: PF00503; G-alpha; 1.
DR PRINTS: PR00318; GPROTEINA.
DR PRODom: PD000281; Gprotein_alpha; 1.
DR SMART: SM00275; G-alpha; 1.
SQ SEQUENCE 355 AA; 41363 MW; 6828C29643F2CE91 CRC64;

Query Match 59.2%; Score 1065.5; DB 5; Length 355;
Best Local Similarity 59.2%; Pred. No. 1.6e-76;
Matches 206; Conservative 53; Mismatches 88; Indels 1; Gaps 1;

QY 5 CCLSAEEKSQISAEIERHVRDKKARRELKLLLLGTGSGKSTFTTKQMRIIHGSGYS 64
DB 3 CLLSEERLQKRINRINRELQDHKDAKKEIKLLLLGTGSGKSTFTTKQMRIIHGSGYS 62
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Db 9 CCPWCLSEDEKAAARVQGEITRLLLEHRRQVRGELKLLLTGSGKSTFKQMRILHGA 68
Qy 62 GYSEDEKRGFTKLVYQNIPTAMQAMIRAMDPLRIQYMCQONKENAQIIREVEVDKVTALS 121
Db 69 GYSEDEKRGFPPLVFNQIFLSVQAIIEAMDRLQIPYRPSKLIHASLVMSQDPYKVNTFE 128
Qy 122 RDQVAAIKQLWLDPGIQFCYDRRREYQSDSAKYIYLDIERIAMPSEVPTQDDVLRVRVP 181
Db 129 TRYALAVQSLWRDAGVRACVERREFHLLDSAVVYLSHLERIAEEGVVPTAQDVLRSMP 188
Qy 182 TTGIIIEYFDELENIIFRMVDVGGGORSERRKWIHCFESVTSIIFLVALSEYDQVLAECNE 241
Db 189 TTGINEYCFVSQKTNLRIVDVGGGKERRKWIHCFEDVTALIFLASLSEYDQCLEENGQE 248
Qy 242 NRMEESKALFRTIITYPWFNLSSVILFNKKDLLEEKIMYSHLISYPEYTGPKQDVKAA 301
Db 249 NRMQESLALGTVLALPWFRTSVILFNKTDILEDKVRTSHLATYFPGFRGPPQDPEAA 308
Qy 302 RDFILKLY-----QDONPD-----KEKVIYSHFTCATDPTNRFVFAAVKDTILOLNL 349
Db 309 KRFILELYTRYAGAAAGPDGASKGPRSRRLFSHYTCATDTONIRKVKVDVRSVLARYL 368
Qy 350 REFNLV 355
Db 369 DEINLL 374
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Job time : 37 secs